

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2731.5	99.3	514	6	ABP72346	Abp72346	Calcineur
2	2524	91.8	487	2	Aaw02536	Calcineur	
3	2524	91.8	487	3	Aab14901	Partial p	
4	2392.5	87.0	524	8	Adj53606	Human kpp	
5	2382	86.6	515	7	ADC99097	Human kpp	
6	2370	86.2	525	7	ADB79777	Rat calci	
7	2100	76.4	400	2	Aaw02537	Calcineur	
8	2057.5	74.8	511	2	AAW57436	Human cal	
9	2057.5	74.8	521	4	ACG67636	Amino aci	
10	2057.5	74.8	521	4	ACG67457	Amino aci	
11	2057.5	74.8	521	8	Adf43224	Human ppp	
12	2057.5	74.8	567	8	ADR66342	Human ppp	
13	2057.5	74.8	567	8	ADR66684	Human pro	
14	2054.5	74.7	456	5	AB309697	Amino aci	
15	2054.5	74.7	511	8	ADF43228	Rat ppp3c	
16	2054.5	74.7	521	5	AB309696	Amino aci	
17	2054.5	74.7	521	8	ADF43226	Mouse ppp	
18	2054.5	74.7	521	8	ADN11631	Calcineur	
19	1992.5	72.5	375	2	Aaw02544	Calcineur	
20	1980.5	72.0	511	8	ADK71833	Human kin	
21	1980.5	72.0	511	8	ABW83040	Human dia	
22	1980.5	72.0	521	8	ABM84824	Human dia	
23	1912	69.5	570	4	ABB64692	Drosophil	
24	1903	69.2	584	4	AB364677	Drosophil	
25	1887.5	68.6	354	2	Aaw02545	Calcineur	



Db 342 LPNFMVFTWSLPPFVGEKVTMLNVLSICSDDELMTGEQDFDVGSAARKEIIRNKIR 401  
Qy 430 AIGKMARVFSVLRESESVLTGKLTPTGMLPSGVLAGGRTQLOSNDVMQLAVPQMDWG 489  
Db 402 AIGKMARVFSVLRESESVLTGKLTPTGMLPSGVLAGGRTQLOSNDVMQLAVPQMDWG 461  
Qy 490 TPHSFANNHNAACREFLFPSSCLSS 515  
Db 462 TTSHFANNTHNACRELLLLFPSSCLSS 487

RESULT 3  
AAB14901  
ID AAB14901 standard; protein; 487 AA.  
AC AAB14901;

DT 08-JAN-2001 (first entry)

XX Partial protein encoded by murine T cell library cDNA clone 11.1.

XX Mouse; calcineurin-binding peptide; A-kinase anchor protein; AKAP;  
KW AKAP 79; immunostimulant; interleukin 2 expression modulation;  
KW graft rejection; transplantation; T cell-mediated disorder.

XX Mus sp.

XX OS

XX US6107104-A.

XX PD 22-AUG-2000.

XX XX 27-SEP-1996; 96US-00721458.

XX PR 23-NOV-1994; 94US-00344227.

XX PR 15-MAR-1995; 95US-00404731.

XX PR 17-JUL-1995; 95US-00503226.

XX XX (ICOS-) ICOS CORP.

XX Lockerbie RO, Gallatin WM, Lai Y, Howard ML;

XX WPI; 2000-578541/54.

XX DR N-PSDB; AAA94251.

XX Novel calcineurin deletion mutant having calcineurin polypeptide sequence

XX and binding A-kinase anchor proteins, for treating graft rejection

XX following organ transplantation and T cell-mediated disorders.

XX Claim 1; Col 53-56; 53pp; English.

XX The present sequence is encoded by clone 11.1 of a murine T cell cDNA

XX library which was subjected to a yeast dihybrid assay using A-kinase

XX anchor protein 79 (AKAP 79) as the bait. The sequence was found to be

XX closely homologous to the human calmodulin dependent protein phosphatase,

XX calcineurin, thus demonstrating that calcineurin binds to AKAP 79.

XX Calcineurin is involved in many intracellular signalling pathways and

XX participates in regulation of IL-2 expression following T cell

XX stimulation in T cells. By binding both cAMP-dependent protein kinase

XX (PKA) and calcineurin, AKAP 79 co-localises a kinase and a phosphatase

XX that may regulate flux through a specific signalling pathway. Calcineurin

XX -binding peptides derived from AKAP 79 may be used to inhibit calcineurin

Matches 480; Conservative 2; Mismatches 4; Indels 20; Gaps 3;  
Qy 11 P P P P P P P P P P G A D R V V K A V P P P T H R L T S E V F D L D G I P R V D V L K N H L V K E G R V D E I A 70  
Db 1 P P P P P P P P P P G A D R V V K A V P P P T H R L T S E V F D M D G I P R V D V L K N H L V K E G R V D E I A 60  
Qy 71 L R I N E G A A I L R R E K T M I E V E A P I T V C G D I H G Q F F D L M K L P E V G G S P A N T R Y L F L G D Y V D 130  
Db 61 L R I N E G A A I L R R E K T M I E V E A P I T V C G D I H G Q F F D L M K L P E V G G S P A N T R Y L F L G D Y V D 120  
Qy 131 R G Y S I E H V L G T E D I S I N P H N N I N E C V L Y L W V L K I L Y P S T L F L L R G N H E C R H L T E Y F T F 190  
Db 121 R G Y F S I ----- E C V L Y L W V L K I L Y P S T L F - L L R G N H E C R H L T E Y F T F 161  
Qy 191 K Q E C K I K Y S E R V Y E A C M E A F D S L P L A A L L N Q Q F L C V H G G L S P E I H T L D D I R R L D R F K E P P 250  
Db 162 K Q E C K I K Y S E R V Y E A C M E A F D S L P L A A L L N Q Q F L C V H G G L S P E I H T L D D I R R L D R F K E P P 221  
Qy 251 A F G M C D L L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F N Y P A V C E F L O N N N L L S I I R A H E 310  
Db 222 A F G M C D L L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F N Y P A V C E F L O N N N L L S I I R A H E 281  
Qy 311 A Q D A G Y R M Y K S Q T T G P P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R O F N C S P H P Y W 370  
Db 282 A Q D A G Y R M Y K S Q T T G P P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R O F N C S P H P Y W 341  
Qy 371 L P N F M D V F T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G E D Q F D - G S A A A R K E I I R N K I R 429  
Db 342 L P N F M D V F T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G E D Q F D V G S A A A R K E I I R N K I R 401  
Qy 430 A I G K M A R V F S V L R E S E S V L T L K G L T P T G M L P S G V L A G G R T Q L O S G N D V M Q L A V P Q M D W G 489  
Db 402 A I G K M A R V F S V L R E S E S V L T L K G L T P T G M L P S G V L A G G R T Q L O S G N D V M Q L A V P Q M D W G 461  
Qy 490 T P H S F A N N H N A C R E F L L F P S S C L S S 515  
Db 462 T T S H F A N N T H N A C R E L L L L F P S S C L S S 487

RESULT 4  
ADJ53606  
ID ADJ53606 standard; protein; 524 AA.  
XX AC ADJ53606;

XX DT 06-MAY-2004 (first entry)

XX Human PPP3CB polypeptide.

XX Human; PPP3CB; antisense oligonucleotide; phosphorothioate linkage;

XX 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;

XX Alzheimer's disease; immunosuppressive; nootropic; neuroprotective;

XX enzyme.

XX Homo sapiens.

XX OS

XX US2004023382-A1.

XX PD 05-FEB-2004.

XX XX 31-JUL-2002; 2002US-00210723.

XX PR 31-JUL-2002; 2002US-00210723.

XX XX (ISIS-) ISIS PHARM INC.

XX Dean NM, Bennett CF, Dobie KW;

XX WPI; 2004-142663/14.

XX DR N-PSDB; ADJ53468.

XX PT New compounds, particularly antisense oligonucleotides targeted to a

XX nucleic acid encoding PPP3CB, useful for treating an autoimmune disorder,

XX

XX

XX

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XX

Query Match 91.8%; Score 2524; DB 3; Length 487;  
Best Local Similarity 94.9%; Pred. No. 1.8e-227;

or Alzheimer's disease.  
 Example 13; SEQ ID NO 4; 91pp; English.

The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding the human PPP3CB polypeptide and inhibits expression of the PPP3CB polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage, i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcytosine. The antisense oligonucleotides are useful for inhibiting expression of the PPP3CB polypeptide and in preparation of a composition for treating autoimmune disorders or Alzheimer's disease. This sequence represents the human PPP3CB polypeptide of the invention.

Sequence 524 AA;

Query Match 87.0%; Score 2392.5; DB 8; Length 524;  
 Best Local Similarity 96.0%; Pred. No. 4.3e-215;  
 Matches 455; Conservative 0; Mismatches 0; Indels 19; Gaps 2;

QY 1 MAAPPARAAPPAPPPPPPPGADRVVKAAPPPTTHRLTSEVFDLGGIPRDVVLKNHLV 60  
 DB 1 MAAPPARAAPPAPPPPPPPGADRVVKAAPPPTTHRLTSEVFDLGGIPRDVVLKNHLV 60  
 QY 61 KEGRVDEEIALRIINEGAAILRRREKTMIEVEAPITVCGDTHGQFFDLMLKLFVGGSPANT 120  
 DB 61 KEGRVDEEIALRIINEGAAILRRREKTMIEVEAPITVCGDTHGQFFDLMLKLFVGGSPANT 120  
 QY 121 RYFLGDDYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLTFLLRGNHE 180  
 DB 121 RYFLGDDYVDRGYFSI-----ECVLYLWVLKILYPSLTFLLRGNHE 161  
 QY 181 CRHLYEFTFKQECKIKYSERVYEAACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 240  
 DB 162 CRHLYEFTFKQECKIKYSERVYEAACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 221  
 QY 241 RRLDRKEPPAFGPMCDLLKSDPSEDFGNEKSQHFHNTVCGSYFYNNVPAVCEFLQNN 300  
 DB 222 RRLDRKEPPAFGPMCDLLKSDPSEDFGNEKSQHFHNTVCGSYFYNNVPAVCEFLQNN 281  
 QY 301 NLLSIIRAHAQAQAGYRMYSKQTTGFPSSLITIFSAFNLDVYNKAAVLKYENNVNIR 360  
 DB 282 NLLSIIRAHAQAQAGYRMYSKQTTGFPSSLITIFSAFNLDVYNKAAVLKYENNVNIR 341  
 QY 361 QFNCSPPHYLWLPNMDVFTWSLPVGEKVTMLVNLVLSICSDDELMTGSDQFDGSAAR 420  
 DB 342 QFNCSPPHYLWLPNMDVFTWSLPVGEKVTMLVNLVLSICSDDELMTGSDQFDGSAAR 401  
 QY 421 KEIIRNKIRAIKGMARVSVLRESESVLTIKGLTPTGMLPSGLVAGGRTQLQS 474  
 DB 402 KEIIRNKIRAIKGMARVSVLRESESVLTIKGLTPTGMLPSGLVAGGRTQLQS 455

RESULT 5  
 ADC99097  
 ID ADC99097 standard; protein; 515 AA.

XX ADC99097;  
 DT 01-JAN-2004 (first entry)  
 XX Human KPP protein - SEQ ID 50.

XX anti-HIV; anti-allergic; anti-inflammatory; antianemic; antiparkinsonian;  
 KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;  
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipeptic;  
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
 KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 KW cancer; developmental; mental retardation; neurological;

Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
 diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 helminthic infection; transgenic; gene therapy; human; enzyme.

Homo sapiens.  
 OS WO2003033680-A2.  
 XX 24-APR-2003.  
 XX 17-OCT-2002; 2002WO-US033723.  
 XX 19-OCT-2001; 2001US-0345474P.  
 XX 02-NOV-2001; 2001US-0343910P.  
 XX 13-NOV-2001; 2001US-0333098P.  
 XX 16-NOV-2001; 2001US-0332424P.  
 XX 30-NOV-2001; 2001US-0334288P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;  
 PI Emerling R, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;  
 PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
 PI Lindquist EA, Lu DAM, Lu Y, Marguis JP, Nguyen DB, Arvizu CS;  
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 PI Zebarradian Y;  
 XX WPI; 2003-403214/38.  
 DR N-PSDB; ADC99149.  
 DR DR  
 XX  
 PT New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.  
 XX  
 PS Claim 1; SEQ ID NO 50; 424pp; English.  
 XX The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.

Query Match 86.6%; Score 2382; DB 7; Length 515;  
 Best Local Similarity 95.8%; Pred. No. 4.1e-214;  
 Matches 455; Conservative 0; Mismatches 0; Indels 20; Gaps 3;

QY 1 MAAPPARAAPPAPPPPPPPGADRVVKAAPPPTTHRLTSEVFDLGGIPRDVVLKNHLV 60  
 DB 1 MAAPPARAAPPAPPPPPPPGADRVVKAAPPPTTHRLTSEVFDLGGIPRDVVLKNHLV 60  
 QY 61 KEGRVDEEIALRIINEGAAILRRREKTMIEVEAPITVCGDTHGQFFDLMLKLFVGGSPANT 120  
 DB 61 KEGRVDEEIALRIINEGAAILRRREKTMIEVEAPITVCGDTHGQFFDLMLKLFVGGSPANT 120  
 QY 121 RYFLGDDYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLTFLLRGNHE 180  
 DB 121 RYFLGDDYVDRGYFSI-----ECVLYLWVLKILYPSLTFLLRGNHE 161  
 QY 181 CRHLYEFTFKQECKIKYSERVYEAACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 240  
 DB 162 CRHLYEFTFKQECKIKYSERVYEAACMEAFDLSPLAALLNQOFLCVHGGLSPEIHTLDDI 221

QY 241 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSOEHFHSHTNVRGCSYFYNYPAVCBFLQNN 300  
 |||||  
 Db 222 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSOEHFHSHTNVRGCSYFYNYPAVCBFLQNN 281  
 |||||  
 QY 301 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 360  
 |||||  
 Db 282 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 341  
 |||||  
 QY 361 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGEDQFD-GSAAA 419  
 |||||  
 Db 342 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGEDQFDVGSAAA 401  
 |||||  
 QY 420 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRQTLOS 474  
 |||||  
 Db 402 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRQTLOS 456  
 |||||  
 RESULT 6  
 ADB79777  
 ID ADB79777 standard; protein; 525 AA.  
 XX  
 AC ADB79777;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Rat calcineurin, A subunit, beta isoform, SEQ ID 17.  
 XX  
 KW Analgesic; pain; streptozocin-induced diabetes; rat.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN EP1279744-A2.  
 XX  
 PD 29-JAN-2003.  
 XX  
 PF 26-JUL-2002; 2002EP-00255249.  
 XX  
 PR 27-JUL-2001; 2001GB-00018354.  
 PR 07-FEB-2002; 2002GB-00002910.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;  
 XX  
 DR WPI; 2003-345407/38.  
 DR N-PSDB; ADB79778.  
 XX  
 PT Use of isolated gene sequences and encoded polypeptides that are  
 PT upregulated in the spinal cord in response to streptozocin-induced  
 PT diabetes for screening compounds for the treatment of pain, or for  
 PT diagnosing pain.  
 XX  
 PS Claim 1; Page 66-67; 334pp; English.  
 XX  
 CC The present invention relates to nucleotide sequences which are useful in  
 CC the screening of compounds for the treatment of pain, or for the  
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the  
 CC spinal cord in response to streptozocin-induced diabetes. The present  
 CC sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 525 AA;  
 Query Match 86.2%; Score 2370; DB 7; Length 525;  
 Best Local Similarity 95.4%; Pred. No. 5.6e-213;  
 Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;  
 QY 1 MAAPEPARAAPPPPPPPPPGADRVKAVPPPPPHRLTSETSEVFDLGDIGIPRVDLKHLV 60  
 |||||  
 Db 1 MAAPEPARAAPPPPPPPPPGADRVKAVPPPPPHRLTSETSEVFDLGDIGIPRVDLKHLV 60  
 |||||  
 QY 61 KEGRVDEBIALRIINEGAAILRREKTMIEVEAPITVCGDIHQFDFLKMFLFEVGGSPANT 120  
 |||||

Db 61 KEGRVDEBIALRIINEGAAILRREKTMIEVEAPITVCGDIHQFDFLKMFLFEVGGSPANT 120  
 |||||  
 QY 121 RYFLGDYVDVDRGYFSIEHVLGTEDISINPHNNINECVLYLWVLYKILYPSLTFLLLRGNHE 180  
 |||||  
 Db 121 RYFLGDYVDVDRGYFSI-----ECVLYLWVLYKILYPSLTFL-LLRGNHE 161  
 |||||  
 QY 181 CRHLYTEYFTFKQECKIKYSERVYEAACMEAFDSLPALALLNQOFLCVHGGLSPEIHTLDDI 240  
 |||||  
 Db 162 CRHLYTEYFTFKQECKIKYSERVYEAACMEAFDSLPALALLNQOFLCVHGGLSPEIHTLDDI 221  
 |||||  
 QY 241 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSOEHFHSHTNVRGCSYFYNYPAVCBFLQNN 300  
 |||||  
 Db 222 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSOEHFHSHTNVRGCSYFYNYPAVCBFLQNN 281  
 |||||  
 QY 301 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 360  
 |||||  
 Db 282 NLLSIIRAHEAQAQAGYMYRKSQTTGFPFSLITIFSAFNLDVYNNKAAVLYKYENNVMNIR 341  
 |||||  
 QY 361 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGEDQFD-GSAAA 419  
 |||||  
 Db 342 QFNCSPPHPVWLPNFMDFVFTWSLPPFVGEKVTEMLVNVLSICSDDELMTEGEDQFDVGSAAA 401  
 |||||  
 QY 420 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRQTLOS 474  
 |||||  
 Db 402 RKEIIRNKIRAIGKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGRQTLOS 456  
 |||||  
 RESULT 7  
 AAW02537  
 ID AAW02537 standard; protein; 400 AA.  
 XX  
 AC AAW02537;  
 XX  
 DT 13-JAN-1997 (first entry)  
 XX  
 DE Calcineurin deletion mutant 1-400.  
 XX  
 KW Autoimmune disease; pACT59; pACT74; pACT36; pACT60; murine; T-cell; PKA;  
 KW mouse; A-kinase anchoring protein 79; cAMP-dependent protein kinase;  
 KW postsynaptic density; AKAP79; human forebrain; transcriptional activator;  
 KW interleukin 2; T-cell activation; calcineurin; T-cell clonal expansion;  
 KW calcium/calmodulin dependent protein phosphatase; T-cell response;  
 KW autoimmune related disease; therapy; immune response.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9616172-A2.  
 XX  
 PD 30-MAY-1996.  
 XX  
 PF 22-NOV-1995; 95WO-US016039.  
 XX  
 PR 23-NOV-1994; 94US-00344227.  
 PR 15-MAR-1995; 95US-00404731.  
 PR 17-JUL-1995; 95US-00503226.  
 XX  
 PA (ICOS-) ICOS CORP.  
 PA (OREG-) STATE OF OREGON.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 XX  
 PI Lockerbie RO, Coghlan VM, Howard ML, Gallatin WM, Scott JD;  
 XX  
 DR WPI; 1996-268608/27.  
 XX  
 PT New modulators of anchoring protein function - used to develop prods. for  
 PT use in the treatment of auto-immune-related conditions.  
 PS Claim 16; Page 7; 74pp; English.  
 XX  
 CC AAW02537-W02556 represent calcineurin (see AAW02536 for full length  
 CC sequence) deletion mutants. Calcineurin is a calcium/calmodulin dependent  
 CC protein phosphatase associated with T-cell activation. Calcineurin is

bound by A-kinase anchoring protein 79 (AKAP79). AKAP79 is responsible for anchoring CAMP-dependent protein kinase (PKA) to specific intracellular sites. AKAP79 is predominantly present in postsynaptic densities in the human forebrain. The pathways that involve AKAP79 are important in many cell types and have been implicated in many cell functions, including the transcriptional activation of the interleukin 2 gene that is important in T-cell activation. By binding both PKA and calcineurin, AKAP79 co-localises a kinase and a phosphatase which may regulate flux through a specific signalling pathway. These sequences can be used in a method for identifying a compound that inhibits binding between an anchor protein (such as AKAP79) and a binding partner. AKAP79 binding sequences can be used to develop products for use in the treatment of autoimmune related conditions. The AKAP79 binding proteins can be used in methods for stimulating an immune response, and for stimulating activated T-cells for selected clonal expansion. The proteins can also be used in a method for enhancing T-cell responses to experimental stimuli for evaluation of early events in T-cell biology and activation of the immune response

XX Sequence 400 AA;

Query Match 76.4%; Score 2100; DB 2; Length 400;  
Best Local Similarity 94.7%; Pred. No. 8.1e-188;  
Matches 397; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

QY 11 P P P P P P P P P G A D R V V K A V P P P P T H R L T S E V F D L G I P R V D V L K N H L V K E G R V D E E I A 70  
D b 1 P P P P P P P P P G A D R V V K A V P P P P T H R L T S E V F D M D G I P R V D V L K N H L V K E G R V D E E I A 60

QY 71 L R I N E G A A I L R R E K T M I E V E A P I T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y V D 130  
D b 61 L R I N E G A A I L R R E K T M I E V E A P I T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y V D 120

QY 131 R G Y S I E H V L G T E D I S I N P H N N I N E C V L Y L W L K I L Y P S T L F L L R G N H E C R H L T E Y T F T F 190  
D b 121 R G Y S I E H V L G T E D I S I N P H N N I N E C V L Y L W L K I L Y P S T L F L L R G N H E C R H L T E Y T F T F 161

QY 191 K O E C K I K Y S E R V Y E A C M E A F D S L P L A A L N Q O F L C V H G G L S P E I H T L D D I R L D R F K E P P 250  
D b 162 K O E C K I K Y S E R V Y E A C M E A F D S L P L A A L N Q O F L C V H G G L S P E I H T L D D I R L D R F K E P P 221

QY 251 A F G P M C D L L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F Y N Y P A V C E F L Q N N L L S I I R A H E 310  
D b 222 A F G P M C D L L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F Y N Y P A V C E F L Q N N L L S I I R A H E 281

QY 311 A Q D A G Y R M Y R K S Q T T G P P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W 370  
D b 282 A Q D A G Y R M Y R K S Q T T G P P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W 341

QY 371 L P N F M D V T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G E D Q F D - G S A A R K E I I R N K I 428  
D b 342 L P N F M D V T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G E D Q F D V G S A A R K E I I R N K I 400

RESULT 8

AAR57436  
ID AAR57436 standard; protein; 511 AA.

XX AAR57436;

DT 18-MAY-1995 (first entry)

DE Human calcineurin A isoform protein.

XX Calcineurin A isoform protein; antibody; diagnosis; identification;  
KW nervous system; tumour.

XX Homo sapiens.

XX JP06181778-A.

XX 05-JUL-1994.

XX

PF 16-DEC-1992; 92JP-00335935.

XX 16-DEC-1992; 92JP-00335935.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI; 1994-251696/31.

XX N-PSDB; AAQ67085.

XX Human calcineurin A alpha isoform protein DNA - useful in study of nerve physiology and biochemistry.

XX Claim 3; Page 9; 14pp; Japanese.

XX The DNA sequence (See AAQ67085) and the encoded protein are useful in research on nerve physiology and biochemistry. The protein may be used to raise antibodies which are useful as diagnostic agents for the

XX identification of nervous system tumours

XX Sequence 511 AA;

Query Match 74.8%; Score 2057.5; DB 2; Length 511;  
Best Local Similarity 83.6%; Pred. No. 1.1e-183;  
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

QY 13 P P P P P P P P P G A D R V V K A V P P P P T H R L T S E V F D L G I P R V D V L K N H L V K E G R V D E E I A L R 72

D b 4 P K A I D P K L S T T D R V V K A V P P P P S H R L T A K E V F D N D G K P R V D I I L K A H L M K S G R U E S V A L R 63

QY 73 I I N E G A A I L R R E K T M I E V E A P I T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y V D R G 132

D b 64 I I T E G A S I L R Q E K N L D I D A P V T V C G D I H G Q F F D L M K L F E V G G S P A N T R Y L F L G D Y V D R G 123

QY 133 Y P S I E H V L G T E D I S I N P H N N I N E C V L Y L W L K I L Y P S T L F L L R G N H E C R H L T E Y T F T F K Q 192

D b 124 Y F S I E H V L G T E D I S I N P H N N I N E C V L Y L W L K I L Y P S T L F L L R G N H E C R H L T E Y T F T F K Q 164

QY 193 E C K I K Y S E R V Y E A C M E A F D S L P L A A L N Q O F L C V H G G L S P E I H T L D D I R L D R F K E P P A F 252

D b 165 E C K I K Y S E R V Y E A C M E A F D S L P L A A L N Q O F L C V H G G L S P E I H T L D D I R L D R F K E P P A Y 224

QY 253 G P M C D L L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F Y N Y P A V C E F L Q N N L L S I I R A H E A Q 312

D b 225 G P M C D L L W S D P S E D F G N E K S Q E H F S H N T V R G C S Y F Y N Y P A V C E F L Q N N L L S I I R A H E A Q 284

QY 313 D A G Y R M Y R K S Q T T G P P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W L P 372

D b 285 D A G Y R M Y R K S Q T T G P P S L I T I F S A P N Y L D V Y N N K A A V L K Y E N N V M N I R Q F N C S P H P Y W L P 344

QY 373 N F M D V F T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G E D Q F D G - S A A R K E I I R N K I R A I 431

D b 345 N F M D V F T W S L P F V G E K V T E M L V N V L S I C S D D E L M T E G E D Q F D G - S A A R K E I I R N K I R A I 403

QY 432 G K M A R V S V L R E E S E S V L T L K G L T P T G M L P S G V L S G G K Q T L Q S 474

D b 404 G K M A R V S V L R E E S E S V L T L K G L T P T G M L P S G V L S G G K Q T L Q S 446

RESULT 9

AAG67636  
ID AAG67636 standard; protein; 521 AA.

XX AAG67636;

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of a human protein.

XX Human; protein kinase; protein phosphatase; signal transduction.

XX Homo sapiens.

XX W0200109316-A1.

```
XX PD 08-FEB-2001.
XX PF
XX PR 28-JUL-2000; 2000WO-JP005061.
XX PR 29-JUL-1999; 99JP-00248036.
XX PR 18-OCT-1999; 99US-0159590P.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 17-FEB-2000; 2000US-0183322P.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PR 09-JUN-2000; 2000JP-00241899.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX PI Senoo C, Nezu J;
XX DR WPI; 2001-570286/64.
XX PT
XX PT New genes encoding proteins with protein kinase/protein phosphatase
XX PT activity, useful in the diagnosis and treatment of diseases.
XX PS Example 4; Page 201-205; 233pp; Japanese.
XX CC The specification describes human protein kinase/protein phosphatases. It
XX CC is expected that the protein kinase/protein phosphatase gene participates
XX CC in signal transduction in cells. The protein kinase/protein phosphatase
XX CC polypeptides and polynucleotides are useful for developing diagnostics
XX CC and treatment agents for human and animal diseases. The protein
XX CC kinase/protein phosphatase polypeptides are useful as target molecules in
XX CC designing novel drugs. The protein kinase/protein phosphatase
XX CC polynucleotides are useful as a source of probes and primers, which may
XX CC be used to isolate homologous sequences. The present sequence represents
XX CC a human protein, which is used in the course of the invention
XX SQ
Sequence 521 AA;
Query Match 74.8%; Score 2057.5; DB 4; Length 521;
Best Local Similarity 83.6%; Pred. No. 1.2e-183;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
QY 13 PPPPPPPPPGADRVVVKAVPPFPPTTHRLTSEEVDLDGIPRDVILKNHLVKEGRVDEIALR 72
DB 4 PKAIDPKLSTTDVVVKAVPPFPSPSHRLTAKEVDNDGKPRVDILKAHLMEGRLEESVALR 63
QY 73 IINEGAAILRRKTMIEWEAPITVCGDIHQGFDMKLFVGGSPANTRYILFLGDYVDRG 132
DB 64 IITEGASILROEKNLIDIDAPVTVCGDTHGQFPDLMKLFVGGSPANTRYILFLGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNINECVLYLWVLKILYPSLTLFLLLRGNHRCRLHTEYFTFKQ 192
DB 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHRCRLHTEYFTFKQ 164
QY 193 ECKIKYSERVYBACMEAFDLSPLAALLNQQLFCVHGGLSPEIHTLDDIRRLDRFKEPPAF 252
DB 165 ECKIKYSERVYDCAWDADFCLPLAALNQQLFCVHGGLSPEIHTLDDIRKLDKRFKEPPAY 224
QY 253 GPMCDLLMSDPSDEFGNKSQHFHSHNTVRGCSYFYNTYPAVCEFLQNNLLSITRAHAQAQ 312
DB 225 GPMCDLLMSDPLEDFGNKTSQHFHSHNTVRGCSYFYSPYPAVCEFLQNNLLSILRAHAQAQ 284
QY 313 DAGYRMYSKQSTGTPSLITIFSAENYLDVYNNKAALVLYNNVNNIRQFNCSPHYWLP 372
DB 285 DAGYRMYSKQSTGTPSLITIFSAENYLDVYNNKAALVLYNNVNNIRQFNCSPHYWLP 344
QY 373 NPMDFVFTWSLPVGEKVTMELVNNLSICSDDELMTEGEQDFG-SAAARKETIRNKIRAI 431
DB 345 NPMDFVFTWSLPVGEKVTMELVNNLSICSDDELMTEGEQDFG-EDGFDGATAAARKEVIRNKIRAI 403
QY 432 GQMARVFSVLRSESVLTGLKGLTPTGMLPGSVLAGGRQTLOS 474
DB 404 GQMARVFSVLRSESVLTGLKGLTPTGMLPGSVLAGGRQTLOS 446
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RESULT 10
AAG67457
XX ID AAG67457 standard; protein; 521 AA.
XX AC AAG67457;
XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of a human polypeptide.
XX KW Human; protein kinase; protein phosphatase; signal transduction;
XX KW intracellular signalling pathway.
XX OS Homo sapiens.
XX PN WO200109345-A1.
XX PD 08-FEB-2001.
XX PF 28-JUL-2000; 2000WO-JP005060.
XX PR 29-JUL-1999; 99JP-00248036.
XX PR 18-OCT-1999; 99US-0159590P.
XX PR 11-JAN-2000; 2000JP-00118776.
XX PR 17-FEB-2000; 2000US-0183322P.
XX PR 02-MAY-2000; 2000JP-00183767.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX PI Senoo C, Nezu J;
XX DR WPI; 2001-564736/63.
XX PT
XX PT New genes encoding protein kinase and protein phosphatase, useful for
XX PT identifying modulators which can be used to treat human or animal
XX PT disorders associated with the expression or function of these enzymes.
XX PS Example 4; Page 301-305; 336pp; Japanese.
XX CC The specification describes human protein kinase/protein phosphatases.
XX CC The polypeptides are expected to participate in signal transduction in
XX CC cells. The kinase phosphatases are connected with intracellular
XX CC signalling pathways. Antisense oligonucleotides and compounds identified
XX CC by screening (agonists or antagonists) can be used to treat human or
XX CC animal disorders associated with the expression or function of the
XX CC protein. In addition, the polypeptides may be used as target molecules
XX CC for drug development. The present sequence represents a polypeptide, used
XX CC in the course of the invention
XX SQ
Sequence 521 AA;
Query Match 74.8%; Score 2057.5; DB 4; Length 521;
Best Local Similarity 83.6%; Pred. No. 1.2e-183;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;
QY 13 PPPPPPPPPGADRVVVKAVPPFPPTTHRLTSEEVDLDGIPRDVILKNHLVKEGRVDEIALR 72
DB 4 PKAIDPKLSTTDVVVKAVPPFPSPSHRLTAKEVDNDGKPRVDILKAHLMEGRLEESVALR 63
QY 73 IINEGAAILRRKTMIEWEAPITVCGDIHQGFDMKLFVGGSPANTRYILFLGDYVDRG 132
DB 64 IITEGASILROEKNLIDIDAPVTVCGDTHGQFPDLMKLFVGGSPANTRYILFLGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNINECVLYLWVLKILYPSLTLFLLLRGNHRCRLHTEYFTFKQ 192
DB 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHRCRLHTEYFTFKQ 164
QY 193 ECKIKYSERVYBACMEAFDLSPLAALLNQQLFCVHGGLSPEIHTLDDIRRLDRFKEPPAF 252
```



Db 165 ECKIKYSERVYDQACMDAFDCLPLAALNNQOFLCVHGGSLSPINTLDDIRKLDREFKEPPAY 224  
Qy 253 GPMCDLLWSDPSEDFGNEKSOEHFHNTRVGCSEFYNNPVCYFELQNNLLSIIRAHEAQ 312  
Db 225 GPMCDLLWSDPLEDFGNEKTOEHFTHTNVRCSEFYSPYPAVCEFLQNNLLSIIRAHEAQ 284  
Qy 313 DAGYRMVRSQTTGFPSPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLP 372  
Db 285 DAGYRMVRSQTTGFPSPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLP 344  
Qy 373 NFMDVFTWSLFPVGEKVTMELVNVLSCSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431  
Db 345 NFMDVFTWSLFPVGEKVTMELVNVLSCSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 403  
Qy 432 GKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGROTLQS 474  
Db 404 GKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGROTLQS 446

RESULT 11  
ID ADF43224 standard; protein; 521 AA.  
XX ADF43224;  
AC ADF43224;  
DT 26-FEB-2004 (first entry)  
XX Human PP3CA amino acid sequence SEQ ID NO:16.  
DE diabetis; pre-diabetic; Type 2 diabetes; diabetes; insulin resistance;  
XX metabolic disease; antidiabetic; human.  
KW Homo sapiens.  
XX  
XX WO2003101284-A2.  
XX  
XX 11-DEC-2003.  
XX  
XX 04-JUN-2003; 2003WO-US017941.  
XX  
XX 04-JUN-2002; 2002US-0385996P.  
PR 04-JUN-2002; 2002US-0386113P.  
PR 06-JUN-2002; 2002US-0386812P.  
PR 06-JUN-2002; 2002US-0386935P.  
PR 06-JUN-2002; 2002US-0386956P.  
PR 06-JUN-2002; 2002US-0386958P.  
PR 06-JUN-2002; 2002US-0387038P.  
XX  
XX (META-) METABOLEX INC.  
XX  
XX Bernard A, Lavan B, Moodie S, Waters S, Wong C;  
XX  
XX WPI; 2004-071055/07.  
DR N-PSDB; ADF43223.  
XX

Identifying an agent for treating diabetes and insulin resistance  
comprising selecting an agent that modulates the expression or activity  
of a polypeptide or that binds to the polypeptide.  
Claim 1; SEQ ID NO 16; 95pp; English.  
XX  
XX The present invention describes a method for identifying an agent for  
XX treating a diabetic or pre-diabetic individual comprising: (a) contacting  
XX an agent to a mixture comprising a polypeptide encoded by a nucleic acid  
XX that hybridises under stringent conditions to a nucleic acid encoding a  
XX sequence comprising the 373 amino acids (ADF43210), 288 amino acids  
XX (ADF43216), 1036 amino acids (ADF43220), 521 amino acids (ADF43224), 913  
XX amino acids (ADF43230), 868 amino acids (ADF43234), 185 amino acids  
XX (ADF43236), or 167 amino acids (ADF43240); and (b) selecting an agent  
XX that modulates the expression or activity of the polypeptide or that  
XX binds to the polypeptide. Also described: (i) treating a diabetic or pre-  
XX diabetic animal; (2) introducing an expression cassette into a cell; (3)  
XX diagnosing an individual who has Type 2 diabetes or is pre-diabetic; (4)

CC an isolated nucleic acid (ADF43233) encoding a polypeptide comprising 868  
CC amino acids (ADF43234); (5) an expression vector comprising the nucleic  
CC acid of (4); and (6) a host cell comprising the expression vector of (5).  
CC The method is useful for identifying an agent for treating a diabetic or  
CC pre-diabetic individual. The agent is useful for diagnosing or treating  
CC diabetes. The polypeptides and modulators of the polypeptides are useful  
CC for diagnosing or treating diabetes, pre-diabetes (including insulin  
CC resistant individuals) and related metabolic diseases. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 521 AA;  
Query Match 74.8%; Score 2057.5; DB 8; Length 521;  
Best Local Similarity 83.6%; Pred. No. 1.2e-183;  
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;  
Qy 13 PPPPPPPPGADRVKAVPPPPPPHRLTSEVFDLGIPIRVDLKHLVKEGRVDEEIALR 72  
Db 4 PKAIDPKLSTTDVVKAVPPPPSHRLTAKEVFDNDGKPRVDILKAHLKMGRLSEVALR 63  
Qy 73 IINEGAAILRREKTMIEVEAPITVCGDIHQFDFLMLKLFVGGSPANTRYLFLGDYVDRG 132  
Db 64 IITEGASILRQEKNLDDIDAPVTCGDIHQFDFLMLKLFVGGSPANTRYLFLGDYVDRG 123  
Qy 133 YFSIEHVLGTEDISINPHNNINECVLYLWLVLPSTLFLLLRGNHECHRLTEYFTFKQ 192  
Db 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHECHRLTEYFTFKQ 164  
Qy 193 ECKIKYSERYVEACMEAFDLSPLAALNNQOFLCVHGGSLSPINTLDDIRKLDREFKEPPAF 252  
Db 165 ECKIKYSERYDQACMDAFDCLPLAALNNQOFLCVHGGSLSPINTLDDIRKLDREFKEPPAY 224  
Qy 253 GPMCDLLWSDPSEDFGNEKSOEHFHNTRVGCSEFYNNPVCYFELQNNLLSIIRAHEAQ 312  
Db 225 GPMCDLLWSDPLEDFGNEKTOEHFTHTNVRCSEFYSPYPAVCEFLQNNLLSIIRAHEAQ 284  
Qy 313 DAGYRMVRSQTTGFPSPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLP 372  
Db 285 DAGYRMVRSQTTGFPSPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLP 344  
Qy 373 NFMDVFTWSLFPVGEKVTMELVNVLSCSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431  
Db 345 NFMDVFTWSLFPVGEKVTMELVNVLSCSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 403  
Qy 432 GKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGROTLQS 474  
Db 404 GKMARVSVLRESESVLTILKGLTPTGMLPSGVLAGGROTLQS 446

RESULT 12  
ADR66342  
ID ADR66342 standard; protein; 567 AA.  
XX  
XX ADR66342;  
AC  
XX  
XX 02-DEC-2004 (first entry)  
DT  
XX  
XX Human prostatic carcinoma derived protein SEQ ID 196 #2.  
DE  
XX  
XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004076614-A2.  
FN  
XX  
XX 10-SEP-2004.  
PD  
XX  
XX 22-FEB-2004; 2004WO-DE000433.  
PF  
XX  
XX 27-FEB-2003; 2003DE-01009985.  
PR  
XX  
XX 14-MAY-2003; 2003DE-01022134.  
PR  
XX



	(HINZ/) HINZWANN B.	271	GPWCIDLLMSDPLEDFGNEKTEQHFHTNTVVRGCSYFYSYPVAVCEFLQHNNLLSILRAHEAQ	333
PA	(DAHL/) DAHL E.			
PA	(ROSE/) ROSENTHAL A.	313	DAGRYMYRKSQTTFPSLITIFSAPNLYDVNNKAVALKYENNVMNIQFNCSPPHYWLP	372
PA	(HERM/) HERMANN K.			
PA	(PILA/) PILARSKY C.	331	DAGRYMYRKSQTTFPSLITIFSAPNLYDVNNKAVALKYENNVMNIQFNCSPPHYWLP	390
XX				
PI	Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;	373	NFMVDFTWSLPPFVGKEKVTMLNVNLISCSDDDELMTEGEDQPG-SAAAKETIRNKIRAI	431
PI	Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;			
PI	Xinzhong L, Staub E;	391	NFMVDFTWSLPPFVGKEKVTMLNVNLISCSDDDELMTEGEDQPG-SAAAKETIRNKIRAI	449
XX				
XX				
XX				
PT	New nucleic acids, and encoded proteins, from prostatic cancer tissue,			
PT	useful for diagnosis, treatment and in screening for specific binding			
PT	agents.			
XX				
XX				
XX				
CC	Claim 2; Page 676; 1607pp; German.			
CC	This invention describes novel cytostatic polynucleotide and polypeptide			
CC	sequences which can be used in a method for diagnosing prostatic cancer			
CC	or the risk of developing prostatic cancer. Diagnosis is based on			
CC	determining over transcription or over expression of the sequences in			
CC	prostatic tissue. Screening for inhibitors of the sequences or detection			
CC	of substances involves a binding assay, any compounds that bind are			
CC	selected, optionally after deconvolution of mixtures. Detection of a			
CC	predetermined minimum level of the reporter indicates the presence of			
CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,			
CC	short-interfering RNA or ribozymes; an organic molecule of molecular			
CC	weight below 5000, preferably 300, that binds to the polypeptide; an			
CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the			
CC	polypeptide, preferably humanised or human; an anti-idiotypic, non-human			
CC	(monoclonal) antibody directed against Ab or any of the above derivatised			
CC	with a reporter group, cell toxin, immunostimulatory molecules and/or			
CC	radioisotope. The polynucleotides are identified in human prostatic			
CC	cancer by differential expression analysis, using DNA microarrays,			
CC	between normal and tumorous tissues, with (over)expression being detected			
CC	by quantitative PCR. Analysis of prostatic cancer samples showed that			
CC	CD24 was upregulated in many of them. Sections of tissue, isolated from			
CC	prostatic cancer patients, or subjects at risk, were incubated			
CC	sequentially with anti-human CD4 murine monoclonal antibodies;			
CC	biotinylated second antibody; streptavidin-conjugated horseradish			
CC	peroxidase and then diaminobenzidine as colour former (brown). The			
CC	samples were counterstained with hemalum (blue). Malignant cells stained			
CC	strongly but non-malignant cells only weakly. In 15 of 63 samples of			
CC	adenocarcinoma, membrane and cytoplasmic staining was very strong, and			
CC	Lymph node metastases were also stained. AD85805-ADR66954 represent the			
CC	polynucleotide and polypeptide sequences used in the method of the			
CC	invention.			
XX				
SQ	Sequence 567 AA;			
	Query Match 74.8%; Score 2057.5; DB 8; Length 567;			
	Best Local Similarity 83.6%; Pred. No. 1.3e-183;			
	Matches 38; Conservative 34; Mismatches 21; Indels 21; Gaps 4;			
Qy	13 PPPPPPPPACRVKXVPFPPTTRILTSEVEFDLDGIPRDVVLKNHVKRGVDBEATLR	72		
Db	50 PKAIDFKLSITDRVKVAFPPFSHRILTAEVFNDNGKPRVDILKAHLMEGRLEESVALR	109		
Qy	73 INEGAAILREKTMTIEVAIPTVCGDIHGQFDLMKLFEVGGSPANTRYLPLDGVDNRG	132		
Db	110 IITEGASILRQENKLLDIADPTVTCGDIHGQFDLMKLFEVGGSPANTRYLPLDGVDNRG	169		
Qy	133 YFSIEHVLTGTDISINPHNNIECVLIYLVWLKILYPSLTFLLRGNHSCRHLTVEYTFKQ	192		
Db	170 YFSI-----ECVLIYLVWLKILYPSLTFLLRGNHSCRHLTVEYTFKQ	210		
Qy	193 ECKIKYSERYVACMAEPDSLPALALLNQOFLCVHGGLSPEITHLDDIRRLDKRKEPPAF	252		
Db	211 ECKIKYSERYVACMAEPDSLPALALLNQOFLCVHGGLSPEINTLDIRDLKRKEPPAY	270		
Qy	253 GPWCIDLLMSDPLEDFGNEKTEQHFHTNTVVRGCSYFYNYPVAVCEFLQHNNLLSILRAHEAQ	312		



ADP43228	
ID	ADP43228 standard; protein; 511 AA.
XX	
AC	ADP43228;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Rat PPP3CA amino acid sequence SEQ ID NO:20.
XX	
KW	diabetic; pre-diabetic; Type 2 diabetes; diabetes; insulin resistance;
KW	metabolic disease; antidiabetic; rat.
XX	
OS	Rattus sp.
XX	
FN	WO2003101284-A2.
XX	
PD	11-DEC-2003;
XX	
PP	04-JUN-2003; 2003WO-US017941.
XX	
PR	04-JUN-2002; 2002US-0385996P.
PR	04-JUN-2002; 2002US-0386113P.
PR	06-JUN-2002; 2002US-0386812P.
PR	06-JUN-2002; 2002US-0386935P.
PR	06-JUN-2002; 2002US-0386956P.
PR	06-JUN-2002; 2002US-0386958P.
PR	06-JUN-2002; 2002US-0387038P.
XX	
PA	(META-) METABOLEX INC.
XX	
PI	Bernard A, Lavan B, Moodie S, Waters S, Wong C;
XX	
DR	WPI; 2004-071055/07.
DR	N-PSDB; ADP43227.
XX	
PT	Identifying an agent for treating diabetes and insulin resistance
PT	comprising selecting an agent that modulates the expression or activity
PT	of a polypeptide or that binds to the polypeptide.
XX	
PS	Disclosure; SEQ ID NO 20; 95pp; English.
XX	
CC	The present invention describes a method for identifying an agent for
CC	treating a diabetic or pre-diabetic individual comprising: (a) contacting
CC	an agent to a mixture comprising a polypeptide encoded by a nucleic acid
CC	that hybridises under stringent conditions to a nucleic acid encoding a
CC	sequence comprising the 373 amino acids (ADP43210), 288 amino acids
CC	(ADP43216), 1036 amino acids (ADP43220), 521 amino acids (ADP43224), 913
CC	amino acids (ADP43230), 868 amino acids (ADP43234), 185 amino acids
CC	(ADP43236), or 167 amino acids (ADP43240); and (b) selecting an agent
CC	that modulates the expression or activity of the polypeptide or that
CC	binds to the polypeptide. Also described: (1) treating a diabetic or pre-
CC	diabetic animal; (2) introducing an expression cassette into a cell; (3)
CC	diagnosing an individual who has Type 2 diabetes or is pre-diabetic; (4)
CC	an isolated nucleic acid (ADP43233) encoding a polypeptide comprising 868
CC	amino acids (ADP43234); (5) an expression vector comprising the nucleic
CC	acid of (4); and (6) a host cell comprising the expression vector of (5).
CC	The method is useful for identifying an agent for treating a diabetic or
CC	pre-diabetic individual. The agent is useful for diagnosing or treating
CC	diabetes. The polypeptides and modulators of the polypeptides are useful
CC	for diagnosing or treating diabetes, pre-diabetes (including insulin
CC	resistant individuals) and related metabolic diseases. The present
CC	sequence is used in the exemplification of the present invention.
XX	
SQ	Sequence 511 AA;

Query Match	74.7%; Score 2054.5; DB 8; Length 511;
Best Local Similarity	83.4%; Pred. No. 2.2e-183;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;	
Qy	13 PPPPPPPGADRVVKA VPPPPHRLTSEEVFDLDGIPRVVDLVKHLVKGSRVDEIALR 72
Db	4 PKAIDPKLSTTDVVVKA VPPPPHRLTSEEVFDLDGIPRVVDLVKHLVKGSRVDEIALR 63

Search completed: February 26, 2005, 14:24:49  
Job time : 178.927 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2392.5	87.0	524	1	P2BB_HUMAN	P16299 homo sapien
2	2389.5	86.9	524	2	Q8HZM9	Q8HZM9 oryctolagus
3	2382	86.6	515	2	Q8N3W4	Q8N3W4 homo sapien
4	2382	86.6	525	1	Q8N1F0	Q8N1F0 homo sapien
5	2370	86.2	525	1	P2BB_MOUSE	P48453 mus musculus
6	2370	86.2	525	1	P2BB_RAT	P20651 rattus norv
7	2060.5	74.9	504	2	Q7T1F5	Q7T1F5 gallus gall
8	2057.5	74.8	511	2	Q8TAW9	Q8TAW9 homo sapien
9	2057.5	74.8	511	2	Q8HZN0	Q8HZN0 oryctolagus
10	2057.5	74.8	521	1	P2BA_HUMAN	Q08209 homo sapien
11	2056.5	74.8	521	1	P2BA_BOVIN	P48452 bos taurus
12	2054.5	74.7	511	2	Q9WUV7	Q9WUV7 rattus norv
13	2054.5	74.7	521	1	P2BA_MOUSE	P63328 mus musculus
14	2054.5	74.7	521	1	P2BA_RAT	P63329 rattus norv
15	2052.5	74.6	511	2	Q95MZ3	Q95M23 sus scrofa
16	2051.5	74.6	511	2	Q6AXB0	Q6AXB0 xenopus lae
17	2047.5	74.5	508	2	Q9DEF7	Q9DEF7 xenopus lae
18	2047.5	74.5	518	2	Q801N4	Q801N4 xenopus lae
19	2006	72.9	507	2	Q61R94	Q61R94 xenopus lae
20	1998.5	72.7	518	2	O5Y438	O5Y438 xenopus lae
21	1985	72.2	502	1	P2BC_HUMAN	P48454 homo sapien
22	1985	72.2	502	2	Q9H4M5	Q9H4M5 homo sapien
23	1985	72.2	512	2	Q9BSG6	Q9BS66 homo sapien
24	1924	70.0	538	2	Q80XK0	Q80XK0 mus musculus
25	1919.5	69.8	513	1	P2BC_MOUSE	P48455 mus musculus
26	1918.5	69.8	506	2	O6AYJ0	O6AYJ0 rattus norv
27	1912.5	69.5	524	2	O7PKK6	O7PKK6 anopheles g
28	1912	69.5	486	2	Q9NKN8	Q9NKN8 patinopecte
29	1912	69.5	570	2	Q9VXF2	Q9VXF2 drosophila
30	1904.5	69.3	485	2	Q9D5R5	Q9D5R5 mus musculus
31	1903	69.2	578	2	Q2T573	Q2T573 drosophila



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QY 421 KEIIRNKIRAIKGMARVSVLRSESVLTGLKLTPTGMLPSGVLAGGRQTLOS 474
Db 402 KEIIRNKIRAIKGMARVSVLRSESVLTGLKLTPTGMLPSGVLAGGRQTLOS 455

RESULT 3
QBN3W4
ID QBN3W4 PRELIMINARY; PRT; 515 AA.
AC QBN3W4;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Protein phosphatase 3 catalytic subunit beta3 (EC 3.1.3.16).
GN Name=PPP3CB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Cohen P.T.W.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AJ48506; CAD32694.1; -.
DR HSSP; Q08209; IAU1.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_ptase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_ptase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 515 AA; 58081 MW; A6762D9468A09B51 CRC64;

Query Match 86.6%; Score 2382; DB 2; Length 515;
Best Local Similarity 95.8%; Pred. No. 2.7e-172;
Matches 455; Conservative 0; Mismatches 0; Indels 20; Gaps 3;

QY 1 MAAPPARAAPPAPPPPPGADRVKAVFPFPHRLTSBEVFDLGIPIVDVLKHLV 60
Db 1 MAAPPARAAPPAPPPPPGADRVKAVFPFPHRLTSBEVFDLGIPIVDVLKHLV 60

61 KEGRVDEIARIINEGAAILREKTMLEVEAPITVCGDIHQCFDMLKLEVGGSANT 120
61 KEGRVDEIARIINEGAAILREKTMLEVEAPITVCGDIHQCFDMLKLEVGGSANT 120

121 RYFLGDVVDGRGYFSIEHVLGTEDISINPHNINECVLYLWVLTLYPSTLFLILRGHNE 180
121 RYFLGDVVDGRGYFSI-----ECVLYLWVLTLYPSTLFLILRGHNE 161

181 CRHLTEYFTFKQCKIKYSERYVEACMEAFDSLPALALNQOFLCVHGLGLSPEIHTLDDI 240
162 CRHLTEYFTFKQCKIKYSERYVEACMEAFDSLPALALNQOFLCVHGLGLSPEIHTLDDI 221

241 RLRLRFKPPAFGPMCDLLWSDSDFCGNEKSHQEHFNTVRCGSFYFNPVAVCEFLQNN 300
222 RLRLRFKPPAFGPMCDLLWSDSDFCGNEKSHQEHFNTVRCGSFYFNPVAVCEFLQNN 281

301 NLLSIIRAHEAQDAGYRMYRSQTTGFPSPITIFSAPNYLDVYNNKAAVLKYENNVNMR 360

Db 421 KEIIRNKIRAIKGMARVSVLRSESVLTGLKLTPTGMLPSGVLAGGRQTLOS 474
Db 402 KEIIRNKIRAIKGMARVSVLRSESVLTGLKLTPTGMLPSGVLAGGRQTLOS 455

RESULT 4
QBN1F0
ID QBN1F0 PRELIMINARY; PRT; 525 AA.
AC QBN1F0;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Protein phosphatase 3 (Formerly 2B), catalytic subunit, beta isoform
DE (Calcineurin A beta).
GN Name=PPP3CB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski W.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; BC028049; AAH28049.1; -.
DR HSSP; Q08209; IAU1.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_ptase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_ptase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 525 AA; 59123 MW; ADB0ECB75371B574 CRC64;

Query Match 86.6%; Score 2382; DB 2; Length 525;
Best Local Similarity 95.8%; Pred. No. 2.7e-172;
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FT METAL 127 Iron and zinc (By similarity).  
 FT METAL 159 Zinc (By similarity).  
 FT ACT SITE 160 Proton donor (By similarity).  
 FT METAL 208 Zinc (By similarity).  
 FT METAL 230 Zinc (By similarity).  
 FT VARSPIC 387 MTEGSDQDVGSAARKEII -> GSEEDGFDGATAARKE  
 VI (in isoform 1).  
 FT 481 /FTID=VSP\_011856.  
 FT CONFLICT 481 E -> G (in Ref. 2).  
 FT CONFLICT 523 SA -> TP (in Ref. 2).  
 SQ SEQUENCE 525 AA; 59173 MW; 5E73BA3100BE2337 CRC64;

Query Match 86.2%; Score 2370; DB 1; Length 525;  
 Best Local Similarity 95.4%; Pred. No. 2.2e-171;  
 Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

QY 1 MAAPPARAAAPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDLGI PRVDVLKHLV 60  
 DB 1 MAAPPARAAAPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDLGI PRVDVLKHLV 60  
 QY 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQFDFDLMLKLFVGGSPANT 120  
 DB 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQFDFDLMLKLFVGGSPANT 120  
 QY 121 RYFLGVDYVDRGYFSIIEHVLGTEDISINPHNNINECVLYLVWLKILYPSITFLLLRGNH 180  
 DB 121 RYFLGVDYVDRGYFSI-----ECVLYLVWLKILYPSITFL-LLRGNH 161  
 QY 181 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHTLDDI 240  
 DB 162 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHTLDDI 221  
 QY 241 RRLDRFKEPPAFGPMCDLLWSDPSDFGNEKSHQSFHSHNTVRGCSYFYNNPAVCEFLQNN 300  
 DB 282 NLLSIIRAHAQDAGYRMYKSSQTTGFPPLITIFSAPNYLDVYNNKAAVLKYENNVNIR 341  
 QY 361 QFNCSPHYPLNFMVDVTSIIPFVGEKVTMLVNLVSLICSDDELMTEGEOFD-GSAAA 419  
 DB 342 QFNCSPHYPLNFMVDVTSIIPFVGEKVTMLVNLVSLICSDDELMTEGEOFDVGSAAA 401  
 QY 420 RKEIIRNKIRAIKGMARVSVLRESESVLTIKGLTPTGMLPSGVLAGGRTQLQS 474  
 DB 402 RKEIIRNKIRAIKGMARVSVLRESESVLTIKGLTPTGMLPSGVLAGGRTQLQS 456

RESULT 6  
 P2BB RAT  
 ID P2BB RAT STANDARD; PRT; 525 AA.  
 AC P20651.  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Serine/threonine protein phosphatase 2B catalytic subunit, beta isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit, beta isoform) (CAM-PRP catalytic subunit).  
 DE Name=Pp3cb;  
 GN Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90121248; PubMed=2558657;  
 RA Kuno T., Takeda T., Hirai M., Ito A., Mukai H., Tanaka C.;  
 RT "Evidence for a second isoform of the catalytic subunit of calmodulin-dependent protein phosphatase (calcineurin A)".  
 RL Biochem. Biophys. Res. Commun. 165:1352-1358(1989).  
 CC -!- FUNCTION: Calcium-dependent, calmodulin-stimulated protein phosphatase. This subunit may have a role in the calmodulin

activation of calcineurin.  
 -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.  
 -!- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By similarity).  
 -!- SUBUNIT: Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity.  
 -!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.

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EMBL; M31809; AAA40848.1; -.  
 EMBL; D90036; BAA14084.1; -.  
 PIR; A33794; A33794.  
 HSSP; Q08209; 1AUI.  
 RGD; 3383; Pp3cb.  
 InterPro; IPR004843; M-pestase.  
 InterPro; IPR006186; T\_phtase\_apah.  
 Pfam; PF00149; Metallophos; 1.  
 PRINTS; PR00114; STPHPTASE.  
 ProDom; PD000252; T\_phtase\_1.  
 SMART; SM00156; PP2AC; 1.  
 SMART; SM00156; PP2AC; 1.  
 PROSITE; PS00125; SSR\_THR\_PHOSPHATASE; 1.  
 Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family;  
 Protein phosphatase; Zinc.  
 DOMAIN 1 310 Catalytic.  
 DOMAIN 11 20 Poly-Pro.  
 DOMAIN 256 362 Calcineurin B binding-site 1 (Potential).  
 DOMAIN 305 310 Calcineurin B binding-site 2 (Potential).  
 DOMAIN 402 424 Calmodulin-binding (Potential).  
 DOMAIN 475 497 Inhibitory domain.  
 METAL 99 99 Iron (By similarity).  
 METAL 101 101 Iron (By similarity).  
 METAL 127 127 Iron and zinc (By similarity).  
 METAL 159 159 Zinc (By similarity).  
 ACT SITE 160 160 Proton donor (By similarity).  
 METAL 208 208 Zinc (By similarity).  
 METAL 290 290 Zinc (By similarity).  
 SEQUENCE 525 AA; 59113 MW; 5E66AF3100BE3987 CRC64;

Query Match 86.2%; Score 2370; DB 1; Length 525;  
 Best Local Similarity 95.4%; Pred. No. 2.2e-171;  
 Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

QY 1 MAAPPARAAAPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDLGI PRVDVLKHLV 60  
 DB 1 MAAPPARAAAPPPPPPPGADRVKAVKAVPPPPHRLTSEVFDLGI PRVDVLKHLV 60  
 QY 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQFDFDLMLKLFVGGSPANT 120  
 DB 61 KEGRVDEIALRIINEGAAILRREKTMIEVEAPITVCGDIHQFDFDLMLKLFVGGSPANT 120  
 QY 121 RYFLGVDYVDRGYFSIIEHVLGTEDISINPHNNINECVLYLVWLKILYPSITFLLLRGNH 180  
 DB 121 RYFLGVDYVDRGYFSI-----ECVLYLVWLKILYPSITFL-LLRGNH 161  
 QY 181 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHTLDDI 240  
 DB 162 CRHLYTEYTFKQECKIKYSERYVEACMEAPDSLPALALNQOFLCVHGLSPETHTLDDI 221  
 QY 241 RRLDRFKEPPAFGPMCDLLWSDPSDFGNEKSHQSFHSHNTVRGCSYFYNNPAVCEFLQNN 300  
 DB 222 RRLDRFKEPPAFGPMCDLLWSDPSDFGNEKSHQSFHSHNTVRGCSYFYNNPAVCEFLQNN 281  
 QY 301 NLLSIIRAHAQDAGYRMYKSSQTTGFPPLITIFSAPNYLDVYNNKAAVLKYENNVNIR 360  
 DB 301 NLLSIIRAHAQDAGYRMYKSSQTTGFPPLITIFSAPNYLDVYNNKAAVLKYENNVNIR 360

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Db 282 NLLSIIRAHAQDAGYMYRSQTTGFPSSLITIFSAFNLDVYNNKAVALKYENNVNIR 341
Qy 361 QFNCSPHYWLPNFMVDVFTWSLPLPVGKVKTEMLVNVLSICSDDELMTGEDEQFD-GSAAA 419
Db 342 QFNCSPHYWLPNFMVDVFTWSLPLPVGKVKTEMLVNVLSICSDDELMTGEDEQFDVGSAAA 401
Qy 420 RKEIIRNKIRAIGKQKARVSVLRESESVLTGKLTPTGMLPSGVLAGGRQTLQS 474
Db 402 RKEIIRNKIRAIGKQKARVSVLRESESVLTGKLTPTGMLPSGVLAGGRQTLQS 456

RESULT 7
Q7TIF5
ID Q7TIF5 PRELIMINARY; PRT; 504 AA.
AC Q7TIF5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciureurin A alpha (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Liberatore C.M., Yutzey K.E.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
    phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AY244634; AA923282.1; -.
DR HSP; Q08209; IAU1.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:phosphatase.
DR Pfam; PF00149; Metallophos; _apah.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
FT NON TER 1
SQ SEQUENCE 504 AA; 56913 MW; 17964C2818765BC5 CRC64;

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Query Match 74.9%; Score 2060.5; DB 2; Length 504;
Best Local Similarity 85.4%; Pred. No. 6.8e-148;
Matches 386; Conservative 33; Mismatches 12; Indels 21; Gaps 4;

Qy 24 DRVVKAVFPFPTHLRTSEVFDLGIPIRVDVLKNHLVKEGRVDEIARLIINEGAATLR 83
Db 9 DRVVKAVFPFPHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASTLRQ 68

Qy 84 EKTMIIEAPITVCGDIGHGQFFDLMLKLFVEVGGSPANTRYFLGDYVDRGVFSIEHVLGTE 143
Db 69 EKNLDDIDAPVTVCGDIGHGQFFDLMLKLFVEVGGSPANTRYFLGDYVDRGVFSI----- 121

Qy 144 DISINPHNNNECVLYLWLVKILYPTSLFLLLRGNHECRHLTEYFTPKQECKIKYSRVY 203
Db 122 -----ECVLYLWLVKILYPTKTLF-LLRGNHECRHLTEYFTPKQECKIKYSRVY 169

Qy 204 EACWEAFDSLPALALLNQQLCVHGGSLPEIHTLDDIRLDRFKEPPAFGPMCDLLWSDP 263
Db 170 DACMDAFDCPLAALMNQQLCVHGGSLPEINTLDDIRLDRFKEPPAFGPMCDLLWSDP 229

Qy 264 SEDFGNEKSOEHFSHTNVRGGSFYFNYPVACEFLQNNLLSIIRAHAQDAGYMYRKSQ 323
Db 230 LEDFGNEKTOEHFTNVRGGSFYFYPVACEFLQNNLLSIIRAHAQDAGYMYRKSQ 289

Qy 324 TTGFPSSLITIFSAFNLDVYNNKAVALKYENNVNIRQFNCSPHYWLPNFMVDVFTWSLP 383
Db 290 TTGFPSSLITIFSAFNLDVYNNKAVALKYENNVNIRQFNCSPHYWLPNFMVDVFTWSLP 349

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Qy 384 FVGEKVTMLVNVLSICSDDELMTGEDEQFDG-SAAARKEIIRNKIRAIGKQKARVSVL 442
Db 350 FVGEKVTMLVNVLSICSDDELGTE-EDGFGATAARKEIIRNKIRAIGKQKARVSVL 408
Qy 443 EESESVLTGKLTPTGMLPSGVLAGGRQTLQS 474
Db 409 EESESVLTGKLTPTGMLPSGVLAGGRQTLQS 440

RESULT 8
Q8TAW9
ID Q8TAW9 PRELIMINARY; PRT; 511 AA.
AC Q8TAW9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PPP3CA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
    Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
    Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
    Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
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    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
    Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
    Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
    Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
    Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
    and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
    phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; BC025714; AAH25714.1; -.
DR HSP; Q08209; IM63.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:phosphatase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 511 AA; 57658 MW; B1E98CC0D6034CCC CRC64;

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Query Match 74.8%; Score 2057.5; DB 2; Length 511;
Best Local Similarity 83.6%; Pred. No. 1.2e-147;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

Qy 13 PPPPPPPPGADRVKAVFPFPTHLRTSEVFDLGIPIRVDVLKNHLVKEGRVDEIARL 72
Db 4 PKAIDPKLSTTDVVKAVFPFPHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALR 63

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QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLFLLLRGNHCHRLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWALKILYPTKTLF-LLRGNHCHRLTEYFTPKQ 164
QY 193 ECKIKYSRVYEAACMEAFDLSPLAALLNQOFLCVHGGSLSPETHTLDDIRRLDRFKPEPPAF 252
DB 165 ECKIKYSRVYDAMDADFCLPLAALMNQOFLCVHGGSLSPETHTLDDIRRLDRFKPEPPAF 224
QY 253 GPMCDLLWSDPSDFGNEKSHQEHFHNTRVRCGSYPYPAVCEFLQNNLLSIIRAHBAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTHQEHFHNTRVRCGSYPYPAVCEFLQNNLLSIIRAHBAQ 284
QY 313 DAGRYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIQFNCSPHPYWLP 372
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QY 373 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG-SAAARKEIIRNKIRAI 403
QY 432 GKMARVFSVLRSESVLTLKGLTPTGMLPSGLVAGSGRTLQS 474
DB 404 GKMARVFSVLRSESVLTLKGLTPTGMLPSGLVAGSGRTLQS 446

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AC Q8HZN0;
DT 01-MAR-2003 (TRENDELrel. 23, Created)
DT 01-MAR-2003 (TRENDELrel. 23, Last sequence update)
DE Calcieneurin A alpha.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22443975; PubMed=12419772;
RA Sun L., Moonga B.S., Lu M., Zaidi N., Iqbal J., Blair H.C.,
RA Epstein S., Abe E., Troen B.R., Huang C.L.H., Zaidi M.,
RT "Molecular cloning, expression, and function of osteoclastic
RT calcieneurin A alpha."
RL Am. J. Physiol. Renal Physiol. 284:F575-F583(2003).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AF541960; AAN23152.1; -.
DR HSSP; Q08209; IM63.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:pesterase.
DR InterPro; IPR006186; T:phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR PRODOM; PD000252; T:phatase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 511 AA; 57655 MW; B1P28D70C7F34CCC CRC64;

Query Match 74.8%; Score 2057.5; DB 2; Length 511;
Best Local Similarity 83.6%; Pred. No. 1.2e-147;
Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPGADRVVKAVPFPPTHLTSEEVFDLGIIPRDVVLKHLVKEGRVDEIAR 72
DB 4 PKAIDPKLSTTDVVVKAVPFPFPPTHLTSEEVFDLGIIPRDVVLKHLVKEGRVDEIAR 63
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QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANTRYLFLGSDYVDRG 132
DB 64 IITEGASILRQEKNLDDIDAPVTVCDDIHGQFFDLMLKLFVGGSPANTRYLFLGSDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPSLFLLLRGNHCHRLTEYFTPKQ 192
DB 124 YFSI-----ECVLYLWALKILYPTKTLF-LLRGNHCHRLTEYFTPKQ 164
QY 193 ECKIKYSRVYEAACMEAFDLSPLAALLNQOFLCVHGGSLSPETHTLDDIRRLDRFKPEPPAF 252
DB 165 ECKIKYSRVYDAMDADFCLPLAALMNQOFLCVHGGSLSPETHTLDDIRRLDRFKPEPPAF 224
QY 253 GPMCDLLWSDPSDFGNEKSHQEHFHNTRVRCGSYPYPAVCEFLQNNLLSIIRAHBAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTHQEHFHNTRVRCGSYPYPAVCEFLQNNLLSIIRAHBAQ 284
QY 313 DAGRYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIQFNCSPHPYWLP 372
DB 285 DAGRYMYRKSQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIQFNCSPHPYWLP 344
QY 373 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG-SAAARKEIIRNKIRAI 403
QY 432 GKMARVFSVLRSESVLTLKGLTPTGMLPSGLVAGSGRTLQS 474
DB 404 GKMARVFSVLRSESVLTLKGLTPTGMLPSGLVAGSGRTLQS 446

RESULT 10
P2BA HUMAN
ID P2BA HUMAN STANDARD; PRT; 521 AA.
AC Q08209;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine/threonine protein phosphatase 2B catalytic subunit, alpha
DE isoform (BC 3.1.3.16) [Calmodulin-dependent calcineurin A subunit,
DE alpha isoform] (CAM-PRP catalytic subunit).
GN Name=PPP3CA; Synonyms=CALNA, CNA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=93320118; PubMed=8392375; DOI=10.1016/0167-4889(93)90117-8;
RA Muramatsu T., Kincaid R.L.;
RT "Molecular cloning of a full-length cDNA encoding the catalytic
RT subunit of human calmodulin-dependent protein phosphatase (calcineurin
RT A alpha).";
RL Biochim. Biophys. Acta 1178:117-120(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Amalgam;
RA Ansonge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;
RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,
RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.,
RA Gasquet L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,
RA Bacquet R., Villafranca J.E.;
RT "Crystal structures of human calcineurin and the human FKBP12-PK506-
RT calcineurin complex."
RL Nature 378:641-644(1995).
CC -1- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
CC phosphatase. This subunit may have a role in the calmodulin
CC activation of calcineurin.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
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phosphate.  
 -1- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit.  
 -1- SUBUNIT: Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity.  
 -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.  
 -----  
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 EMBL; L14778; AAA02631.1; -.  
 DR EMBL; AL353950; CAB89253.1; -.  
 DR PIR; S35067; S35067.  
 DR PDB; 1AUI; X-ray; A=1-426.  
 DR PDB; 1M63; X-ray; A/B=1-372.  
 DR PDB; 1MF8; X-ray; A=20-392.  
 DR GeneW; HGNC:9314; PPP3CA.  
 DR H-InvDB; HIX0004409; -.  
 DR MIM; 114105; -.  
 DR GO; GO:0005955; C:calcineurin complex; NAS.  
 DR GO; GO:0005509; F:calcium ion binding; NAS.  
 DR GO; GO:0005516; F:calmodulin binding; NAS.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; NAS.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; NAS.  
 DR InterPro; IPR004843; M-peptidase.  
 DR InterPro; IPR006186; T-phatase\_apah.  
 DR Pfam; PF00149; Metallophos; 1.  
 DR PRINTS; PR00114; STPHPTASE.  
 DR ProDom; PD000252; T\_phatase\_apah; 1.  
 DR SMART; SM00156; PP2Ac; 1.  
 DR PROSITE; PS00125; SER\_THR\_PHOSPHATASE; 1.  
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 KW Multigene family; Protein phosphatase; Zinc.  
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 Query Match 74.8%; Score 2057.5; DB 1; Length 521;  
 Best Local Similarity 83.6%; Pred. No. 1.2e-147;  
 Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;  
 QY 13 PPPPPPPPGADRVKAVPPPPPHRLTSEVFDLDGI PRVDVLKHLVKEGRVDEEIALR 72  
 DB 4 PKAIDPKLSTTDVWKAVPPPPSHRLTAKEVFNDGKPRVDILKAHLMKEGRLEESVALR 63  
 QY 73 IINEGRAILRRKTMIEVEAPITVCGDIHQFFDLMLKEVGGSPANTRYFLGDDVYDRG 132  
 DB 64 IITEGASILRQEKNNLLDIDAPVTVCGDIHQFFDLMLKEVGGSPANTRYFLGDDVYDRG 123  
 QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVLKILYPTSLFLLRGNHCEHRLTEYFTFKQ 192  
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 QY 432 GKMARVFSVLRRESESVLTILKGLTPTGMLPSGVLAGSGROTLOS 474  
 DB 404 GKMARVFSVLRRESESVLTILKGLTPTGMLPSGVLAGSGKQTLOS 446  
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 P2BA\_BOVIN

P2BA BOVIN STANDARD; PRT; 521 AA.  
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 01-FEB-1996 (Rel. 33, Created)  
 01-FEB-1996 (Rel. 33, Last sequence update)  
 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Serine/threonine protein phosphatase 2B catalytic subunit, alpha isoform (EC:3.1.3.16) (Calmodulin-dependent calcineurin A subunit, alpha isoform (EC:3.1.3.16) (CAM-PRP catalytic subunit)).  
 DE alpha isoform (EC:3.1.3.16) (Calmodulin-dependent calcineurin A subunit, alpha isoform (EC:3.1.3.16) (CAM-PRP catalytic subunit)).  
 GN Name=PPP3CA;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RC TISSUE=Brain;  
 RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;  
 RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A., Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;  
 RT "X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FKBP12-FK506 complex."; Cell 82:507-522(1995).  
 RL Cell 82:507-522(1995).  
 CC -!- FUNCTION: Calcium-dependent, calmodulin-stimulated protein phosphatase. This subunit may have a role in the calmodulin activation of calcineurin.  
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.  
 CC -!- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit.  
 CC -!- SUBUNIT: Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity.  
 CC -!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U33868; AAC48473.1; -;  
 CC PIR; A56968; A56968.  
 CC PDB; LTCO; X-ray; A-18-392.  
 CC InterPro; IPR004843; M-pesterase.  
 CC InterPro; IPR006186; T\_phthase\_apah.  
 CC Pfam; PF00149; Metallophos; 1.  
 CC PRINTS; PR00114; STPHPTASE.  
 CC ProDom; PD000252; T\_phthase\_apah; 1.  
 CC SMART; SM00156; PP2Ac; 1. PHOSPHATASE; 1.  
 CC PROSITE; PS00125; SER\_THR\_PHOSPHATASE; 1.  
 KW 3D-structure; Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family; Protein phosphatase; Zinc.  
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 KW DOMAIN 296 301 Calcineurin B binding-site 2 (Potential).  
 KW DOMAIN 392 414 Calmodulin-binding (Potential).  
 KW DOMAIN 465 487 Inhibitory domain.  
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 SQ SEQUENCE 521 AA; 58671 MW; F3F153F22AB56BDF CRC64;  
 Query Match 74.8%; Score 2056.5; DB 1; Length 521;  
 Best Local Similarity 83.6%; Pred. No. 1.4e-147;  
 Matches 387; Conservative 34; Mismatches 21; Indels 21; Gaps 4;  
 QY 13 PPPPPPPPGADRVVKAVPFPPTHLTSEEVFDLDGIPRDVLKNHLVKEGRVDEIALR 72  
 DB 4 PKADPKSLTTRDVVKAVPFPFPSPHRLTAKEVFDNDGKPRVDILKAHLMKGRLEETVALR 63  
 QY 73 IINGGAAILREKTMIEVEAPITVCGDHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRG 132  
 DB 64 IITEGASILROEKNLDDIDAPVTVCGDHGFDFDLMKLFEVGGSPANTRYLFLGDYVDRG 123  
 QY 133 YFSIEHVLGTEDISINPHNNINECVLYLVWLKILYPSLFLLLRGNHCRHLTEVTFPKQ 192  
 DB 124 YFSI-----BCVLYLWAKILYPKTLF--LLRGNHCRHLTEVTFPKQ 164  
 QY 193 ECKIKYSERVYEAQWEAFDSLPALANQQLCVHGGSLSPETHTDTRRLDRFKPEPPAF 252  
 DB 165 ECKIKYSERVYDADCAFDCLPLAALNNQQLCVHGGSLSPETHTDTRRLDRFKPEPPAF 224  
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QY 313 DAGYMRKSKQTTFPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWLP 372
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QY 373 NFMDVFTWSLPFFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMDVFTWSLPFFVGEKVTMLVNVLSICSDDELGSE-EDGFDGATAARKEIIRNKIRAI 403
QY 432 GKMARVFSVLRESESVLTGLTPTGMLPSGVLAGGRTQLQS 474
DB 404 GKMARVFSVLRESESVLTGLTPTGMLPSGVLAGGRTQLQS 446

RESULT 12
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ID AC Q9WUV7 PRELIMINARY; PRT; 511 AA.
AC Q9WUV7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine specific protein phosphatase (EC 3.1.3.16).
GN Names=calcineurin A gene;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Antire brain;
RA MEDLINE=92348467; PubMed=1322410;
RX Perrinoo B.A., Fong Y.L., Brickey D.A., Saitoh Y., Ushio Y.,
RA Fukunaga K., Miyamoto E., Soderling I.R.;
RT "Characterization of the phosphatase activity of a Baculovirus-
expressed calcineurin A isoform.";
RL J. Biol. Chem. 267:15965-15969(1992).
CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -|- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; X57115; CAA0398.2; -.
DR HSSP; Q08209; IM63.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004721; F:phosphoprotein phosphatase activity; IEA.
DR InterPro; IPR004843; N-pesterase.
DR InterPro; IPR006186; T_phase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPHASE.
DR PRODOM; PD000252; T_phase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 511 AA; 57614 MW; 01428D70D674508D CRC64;

Query Match 74.7%; Score 2054.5; DB 2; Length 511;
Best Local Similarity 83.4%; Pred. No. 2e-147;
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

QY 13 PPPPPPPPGADRVKAVPPPPHRLTSEVFDLGIIPRVVLKNHLVKEGRVDEIALR 72
DB 4 PKAIDPKLSTTDVRVKAAPPSPSHRLTAKEVFNDGKPRVDILKAHLMEGRLEESVALR 63
QY 73 IINEGAIRLREKTMIEVEAPITVCGDIHQGFEDLMKLFEVGGSPANTRYLFLGDYDRG 132
DB 64 IITEGASILRQENLDDIDAPVTCGDIHQGFEDLMKLFEVGGSPANTRYLFLGDYDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWLKILYPTSTFLLRGNHCEHRLTEYFTFKQ 192
DB 124 YFSI-----ECVLYLWALKILYPTKTLF-LLRGNHCEHRLTEYFTFKQ 164
QY 193 ECKIKYSERYVACMEAFDLSPLAALNQOFLCVHGGLSPEIHTLDDIRLDRFKPEPPAF 252
DB 165 ECKIKYSERYVADCMADFCLPLAALNQOFLCVHGGLSPEINTLDDIRLDRFKPEPPAY 224

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QY 253 GPMCDLLWSDPSDFGNEKSQEHFSHTVRCGSFYFNYPVAVCFEFLONNNLLSIRAHEAQ 312
DB 225 GPMCDLLWSDPLEDFGNEKTOEHFTHTVRCGSFYFYPVAVCDFLOHNNLLSIRAHEAQ 284
QY 313 DAGYMRKSKQTTFPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWLP 372
DB 285 DAGYMRKSKQTTFPSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIRQNCSPHPYWLP 344
QY 373 NFMDVFTWSLPFFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
DB 345 NFMDVFTWSLPFFVGEKVTMLVNVLSICSDDELGSE-EDGFDGATAARKEIIRNKIRAI 403
QY 432 GKMARVFSVLRESESVLTGLTPTGMLPSGVLAGGRTQLQS 474
DB 404 GKMARVFSVLRESESVLTGLTPTGMLPSGVLAGGRTQLQS 446

RESULT 13
P2BA_MOUSE
ID P2BA_MOUSE STANDARD; PRT; 521 AA.
AC P63328; P12816; P20652;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Serine/threonine protein phosphatase 2B catalytic subunit, alpha
isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit,
alpha isoform) (CAM-PRP catalytic subunit).
GN Names=Ppp3ca; Synonyms=Calna;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90293081; PubMed=2162844;
RA Kincaid R.L., Giri P.R., Higuchi S., Tamura J., Dixon S.C.,
RA Marietta C.A., Amores D.A., Martin B.M.;
RT "Cloning and characterization of molecular isoforms of the catalytic
subunit of calcineurin using nonisotopic methods.";
RL J. Biol. Chem. 265:11312-11319(1990).
RN [2]
RP SEQUENCE OF 215-521 FROM N.A.
RX MEDLINE=89057863; PubMed=2848250;
RA Kincaid R.L., Nightingale M.S., Martin B.M.;
RT "Characterization of a cDNA clone encoding the calmodulin-binding
domain of mouse brain calcineurin.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:8983-8987(1988).
RN [3]
RP SEQUENCE OF 95-116 FROM N.A.
RX MEDLINE=94357899; PubMed=8077208;
RA Becker W., Kentrup H., Klumpp S., Schultz J.E., Joost H.G.;
RT "Molecular cloning of a protein serine/threonine phosphatase
containing a putative regulatory tetratricopeptide repeat domain.";
RL J. Biol. Chem. 269:22586-22592(1994).
CC -|- FUNCTION: Calcium-dependent, calmodulin-stimulated protein
phosphatase. This subunit may have a role in the calmodulin
activation of calcineurin.
CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -|- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By
similarity).
CC -|- SUBUNIT: Composed of two components (A and B), the A component is
the catalytic subunit and the B component confers calcium
sensitivity.
CC -|- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B
subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

EMBL; J05479; AAA37359.1; -;  
 EMBL; J04134; AAA37432.1; -;  
 PIR; A42232; A31257.  
 HSSP; Q08209; 1M63.  
 MGD; MGI:107164; Ppp3ca.  
 InterPro; IPR004843; M-pesterase.  
 InterPro; IPR006186; T.phase\_apah.  
 Pfam; PF00114; Metallophos; 1.  
 PRINTS; PR00114; STPHPTASE.  
 ProDom; PD000252; T.phase\_apah; 1.  
 SMART; SM00156; PP2Ac; 1.  
 Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family;  
 Protein phosphatase; Zinc.  
 DOMAIN 1 301  
 FT DOMAIN 247 253  
 FT DOMAIN 296 301  
 FT DOMAIN 392 414  
 FT DOMAIN 465 487  
 FT METAL 90 90  
 FT METAL 92 92  
 FT METAL 118 118  
 FT METAL 150 150  
 FT ACT SITE 151 151  
 FT METAL 199 199  
 FT METAL 281 281  
 SQ SEQUENCE 521 AA; 58643 MW; 16530C27DDBF1F05 CRC64;

Query Match 74.7%; Score 2054.5; DB 1; Length 521;  
 Best Local Similarity 83.4%; Pred. No. 2e-147;  
 Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

13 PPPPPPPGADRVVKA VPPPTTHRLTSEEVDLDGIPRDVILKNHLVKRGVDEIALR 72  
 4 PKAIDPKLSTTDRVVVKA VPPPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLSEVALR 63

73 IINEGAAILREKTMIEVAPTTCGDITHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 132  
 64 IITEGASILRQEKLLDIDAPVTVCGDTHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 123

133 YFSIEHLVLTGDISINPHNNIECVLYLWLKILYPTSLFLLRGNHCEHRLTEYFTFKQ 192  
 124 YFSI-----ECVLYLWLKILYPTKTLF-LLRGNHCEHRLTEYFTFKQ 164

193 ECKIYSRVYEAWEAFDSPLAALLNQFLCVHGGLSPEIHTLDDIRLDRKPEPPAF 252  
 165 ECKIYSRVYDADWDADFCLPLAALMNQFLCVHGGLSPEINTLDDIRLDRKPEPPAY 224

253 GPMCDLLWSDSEDFGNEKSOEHFSHNTVRCGSFYFNPVPAVCEFLQNNLLSIIRAHAQ 312  
 225 GPMCDLLWSDLEDFGNEKSEKTEHFTHTVRCGSFYFNPVPAVCEFLQNNLLSIIRAHAQ 284

313 DAGYMYRKSQTTGPPSLITTFSAFNYLDVYNNKAAVLKYNNVNNIRQFNCSPHYWLP 372  
 285 DAGYMYRKSQTTGPPSLITTFSAFNYLDVYNNKAAVLKYNNVNNIRQFNCSPHYWLP 344

373 NFMVDVFTWSLFPVGEKVTEMLVNVLSICSDDELMTGEDQFDG-SAAARKKIIIRNKIRAI 431  
 345 NFMVDVFTWSLFPVGEKVTEMLVNVLSICSDDELGSE-EDGFGDGAATAARKVIRNKIRAI 403

432 GKMARVFSVLREESVLTGLKLTGMLPSGLVLAGGQTLOS 474  
 404 GKMARVFSVLREESVLTGLKLTGMLPSGLVLAGGQTLOS 446

RESULT 14

P2BA\_RAT

ID P2BA\_RAT STANDARD; PRT; 521 AA.

AC P63329; P12816; P20652;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

25-OCT-2004 (Rel. 45, Last annotation update)  
 Serine/threonine protein phosphatase 2B catalytic subunit, alpha isoform (EC 3.1.3.16) (Calmodulin-dependent calcineurin A subunit, alpha isoform) (CAM-PRP catalytic subunit).  
 Name=Ppp3ca; Synonyms=Calna;  
 Rattus norvegicus (Rat).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=89392066; PubMed=2551293;  
 Ito A., Hashimoto T., Hirai M., Takeda T., Shuntoh H., Kuno T., Tanaka C.;  
 "The complete primary structure of calcineurin A, a calmodulin binding protein homologous with protein phosphatases 1 and 2A.";  
 Biochem. Biophys. Res. Commun. 163:1492-1497(1989).  
 -!- FUNCTION: Calcium-dependent, calmodulin-stimulated protein phosphatase. This subunit may have a role in the calmodulin activation of calcineurin.  
 -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphates. Binds 1 iron(III) ion and 1 zinc ion per subunit (By similarity).  
 -!- COFACTOR: Binds 1 iron(III) ion and 1 zinc ion per subunit (By similarity).  
 -!- SUBUNIT: Composed of two components (A and B), the A component is the catalytic subunit and the B component confers calcium sensitivity (By similarity).  
 -!- SIMILARITY: Belongs to the PPP phosphatase family. PP-2B subfamily.  
 -----  
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 EMBL; M29275; AAA40940.1; -;  
 EMBL; D90035; BAA14083.1; -;  
 PIR; A33264; A33264.  
 HSSP; Q08209; 1M63.  
 RGD; 3382; Ppp3ca.  
 InterPro; IPR004843; M-pesterase.  
 InterPro; IPR006186; T.phase\_apah.  
 Pfam; PF00149; Metallophos; 1.  
 PRINTS; PR00114; STPHPTASE.  
 ProDom; PD000252; T.phase\_apah; 1.  
 SMART; SM00156; PP2Ac; 1.  
 PROSITE; PS00125; SER\_THR\_PHOSPHATASE; 1.  
 Calmodulin-binding; Hydrolase; Iron; Metal-binding; Multigene family;  
 Protein phosphatase; Zinc.  
 DOMAIN 1 301  
 FT DOMAIN 247 253  
 FT DOMAIN 296 301  
 FT DOMAIN 392 414  
 FT DOMAIN 465 487  
 FT METAL 90 90  
 FT METAL 92 92  
 FT METAL 118 118  
 FT METAL 150 150  
 FT ACT SITE 151 151  
 FT METAL 199 199  
 FT METAL 281 281  
 SQ SEQUENCE 521 AA; 58643 MW; 16530C27DDBF1F05 CRC64;

Query Match 74.7%; Score 2054.5; DB 1; Length 521;  
 Best Local Similarity 83.4%; Pred. No. 2e-147;  
 Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;

13 PPPPPPPGADRVVKA VPPPTTHRLTSEEVDLDGIPRDVILKNHLVKRGVDEIALR 72  
 4 PKAIDPKLSTTDRVVVKA VPPPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLSEVALR 63

73 IINEGAAILREKTMIEVAPTTCGDITHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 132  
 64 IITEGASILRQEKLLDIDAPVTVCGDTHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRG 123

133 YFSIEHLVLTGDISINPHNNIECVLYLWLKILYPTSLFLLRGNHCEHRLTEYFTFKQ 192  
 124 YFSI-----ECVLYLWLKILYPTKTLF-LLRGNHCEHRLTEYFTFKQ 164

193 ECKIYSRVYEAWEAFDSPLAALLNQFLCVHGGLSPEIHTLDDIRLDRKPEPPAF 252  
 165 ECKIYSRVYDADWDADFCLPLAALMNQFLCVHGGLSPEINTLDDIRLDRKPEPPAY 224

253 GPMCDLLWSDSEDFGNEKSOEHFSHNTVRCGSFYFNPVPAVCEFLQNNLLSIIRAHAQ 312  
 225 GPMCDLLWSDLEDFGNEKSEKTEHFTHTVRCGSFYFNPVPAVCEFLQNNLLSIIRAHAQ 284

313 DAGYMYRKSQTTGPPSLITTFSAFNYLDVYNNKAAVLKYNNVNNIRQFNCSPHYWLP 372  
 285 DAGYMYRKSQTTGPPSLITTFSAFNYLDVYNNKAAVLKYNNVNNIRQFNCSPHYWLP 344

373 NFMVDVFTWSLFPVGEKVTEMLVNVLSICSDDELMTGEDQFDG-SAAARKKIIIRNKIRAI 431  
 345 NFMVDVFTWSLFPVGEKVTEMLVNVLSICSDDELGSE-EDGFGDGAATAARKVIRNKIRAI 403

432 GKMARVFSVLREESVLTGLKLTGMLPSGLVLAGGQTLOS 474  
 404 GKMARVFSVLREESVLTGLKLTGMLPSGLVLAGGQTLOS 446

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QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRG 132
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Db 64 IITEGASILRQEKNLDDIDAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRG 123
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QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWLVKILYPSLFLLRGNHECHRLTEYFTFKQ 192
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QY 193 ECKIKYSERYVEACMEAFDSPLAALLNQOFLCVHGGSLSPETHTLDDIRLDRFKKEPPAF 252
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Db 165 ECKIKYSERYVYDAMDADFCLPLAALNQOFLCVHGGSLSPETHTLDDIRLDRFKKEPPAY 224
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 253 GPMCDLLWSDPSDFGNEKSHQEHFHTNTRVGCSTFYSPAVCEFLQHNLLSILRAHEAQ 312
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 225 GPMCDLLWSDPLEDFGNEKTHQEHFHTNTRVGCSTFYSPAVCEFLQHNLLSILRAHEAQ 284
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QY 313 DAGYRMYRKSQTTGFPSSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIROQNCSPHPYWLP 372
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QY 373 NFMDVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
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Db 345 NFMDVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 403
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QY 432 GKMARVFSVLRRESSESVLTILKGLTPTGMLPSGVLAGGRTQLQS 474
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Db 404 GKMARVFSVLRRESSESVLTILKGLTPTGMLPSGVLAGGRTQLQS 446
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## RESULT 15

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Q95WZ3
ID Q95M23 PRELIMINARY; PRT; 511 AA.
AC Q95M23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcineurin catalytic subunit delta isoform (EC 3.1.3.16).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Depreux F.F.S., Bidwell C.A.B., Grant A.L., Gerrard D.E.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AF193515; AAK56844.1; -.
DR HSSP; Q08209; 1AUI.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0004721; F:phosphoprotein phosphatase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_ptcase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_ptcase_apah; 1.
DR SMART; SM00156; PP2ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 511 AA; 57636 MW; 7C30BB04B3D2D29 CRC64;
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Query Match 74.6%; Score 2052.5; DB 2; Length 511;
Best Local Similarity 83.4%; Pred. No. 2.8e-147;
Matches 386; Conservative 34; Mismatches 22; Indels 21; Gaps 4;

QY 13 PPPPPPPGADRVRVAVPPPPHRLTSEEVFDLGGIPRVQVVKHVLKESGRVDEETAIR 72
Db ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 PKAIDPKLSTTDRVRVAVPPPPHRLTAKEVFDNDGKPRVDILKAHLMKGRLEENVALR 63
QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRG 132
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Db 64 IITEGASILRQEKNLDDIDAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRG 123
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWLVKILYPSLFLLRGNHECHRLTEYFTFKQ 192
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 124 YFSI-----ECVLYLWALKILYPKTLF-LLRGNHECHRLTEYFTFKQ 164
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 193 ECKIKYSERYVEACMEAFDSPLAALLNQOFLCVHGGSLSPETHTLDDIRLDRFKKEPPAF 252
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Db 165 ECKIKYSERYVYDAMDADFCLPLAALNQOFLCVHGGSLSPETHTLDDIRLDRFKKEPPAY 224
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QY 253 GPMCDLLWSDPSDFGNEKSHQEHFHTNTRVGCSTFYSPAVCEFLQHNLLSILRAHEAQ 312
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QY 313 DAGYRMYRKSQTTGFPSSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIROQNCSPHPYWLP 372
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Db 285 DAGYRMYRKSQTTGFPSSLITIFSAAPNYLDVYNNKAAVLKYENNVMNIROQNCSPHPYWLP 344
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QY 373 NFMDVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 431
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Db 345 NFMDVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDG-SAAARKEIIRNKIRAI 403
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QY 432 GKMARVFSVLRRESSESVLTILKGLTPTGMLPSGVLAGGRTQLQS 474
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Db 404 GKMARVFSVLRRESSESVLTILKGLTPTGMLPSGVLAGGRTQLQS 446
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Search completed: February 26, 2005, 14:28:51  
Job time : 179.927 secs

Result No.	Score	Query #		DB	ID	Description
		Match	Length			
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2	2392.5	87.0	525	2	B36222	phosphoprotein pho
3	2370	86.2	525	1	A33794	phosphoprotein pho
4	2321	84.4	515	2	JT0976	phosphoprotein pho
5	2057.5	74.8	521	1	S35067	phosphoprotein pho
6	2056.5	74.8	521	1	A56968	phosphoprotein pho
7	2054.5	74.7	521	2	A31257	phosphoprotein pho
8	2054.5	74.7	521	2	A33264	phosphoprotein pho
9	1985	72.2	502	1	JC1283	phosphoprotein pho
10	1919.5	69.8	513	2	A38193	phosphoprotein pho
11	1910	69.5	486	1	JC7241	phosphoprotein pho
12	1903	69.2	578	1	S70534	phosphoprotein pho
13	1895.5	68.9	569	1	S70551	phosphoprotein pho
14	1871	68.0	535	1	T18864	phosphoprotein pho
15	1836	66.8	560	2	A47433	phosphoprotein pho
16	1828.5	66.5	577	2	B44307	phosphoprotein pho
17	1592	57.9	554	2	T50310	phosphoprotein pho
18	1586	57.7	554	2	T45137	phosphoprotein pho
19	1548.5	56.3	518	2	A40942	phosphoprotein pho
20	1527.5	55.5	530	2	S46322	phosphoprotein pho
21	1393.5	50.7	623	2	S68963	phosphoprotein pho
22	1300.5	47.3	604	2	S49804	phosphoprotein pho
23	1275	46.4	553	2	S16809	phosphoprotein pho
24	851	30.9	253	2	A0181	phosphoprotein pho
25	744	27.1	255	2	C32222	phosphoprotein pho
26	584.5	21.3	326	2	T09995	phosphoprotein pho
27	582.5	21.2	326	2	T09544	phosphoprotein pho
28	577.5	21.0	310	2	S60471	phosphoprotein pho
29	576.5	21.0	322	1	S31087	phosphoprotein pho

Db 240 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQHFSHTVRGCSYFNYPAVCEFLQNN 299  
Qy 301 NLLSIIRAHEAQDAGYMYRKSQTTGPPSLITIFSAPNYLDVYNNKAALVLYENNVNIR 360  
Db 300 NLLSIIRAHEAQDAGYMYRKSQTTGPPSLITIFSAPNYLDVYNNKAALVLYENNVNIR 359  
Qy 361 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 420  
Db 360 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 419  
Qy 421 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQSGNDVMQ 480  
Db 420 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQSGNDVMQ 479  
Qy 481 LAVPQMDWGTSPHSPANNSHNACREFLFFSSCLSS 515  
Db 480 LAVPQMDWGTSPHSPANNSHNACREFLFFSSCLSS 514

RESULT 2  
B36222  
phosphoprotein phosphatase (EC 3.1.3.16) 3-beta catalytic chain, splice form 2 - human  
N;Alternate names: calcineurin catalytic chain; calcineurin chain A beta; calcineurin ch  
C;Species: Homo sapiens (man)  
C;Date: 04-Oct-1991 #sequence\_revision 13-Jan-1993 #text\_change 16-Aug-2004  
C;Accession: B36222; S14272  
R;Guerini, D.; Klee, C.B.  
A;Title: Cloning of human calcineurin A: evidence for two isozymes and identification of  
A;Reference number: A36222; MUID:90083232; PMID:2556704  
A;Accession: B36222  
A;Molecule type: mRNA  
A;Residues: 1-524 <GUE>  
A;Cross-references: UNIPROT:P16299; GB:M29551; NID:g180708; PIDN:AAA35706.1; PID:g180709  
R;McPartlin, A.E.; Barker, H.M.; Cohen, P.T.W.  
Biochim. Biophys. Acta 1088, 308-310, 1991  
A;Title: Identification of a third alternatively spliced cDNA encoding the catalytic sub  
A;Reference number: S14272; MUID:91159485; PMID:1848109  
A;Accession: S14272  
A;Molecule type: mRNA  
A;Residues: 1-395, 'V', 396-456, 467-524 <MCP>  
C;Genetics:  
A;Gene: GDB:PPP3CB  
A;Cross-references: GDB:I31362; OMIM:114106  
A;Map position: 10q21-10q22  
C;Complex: heterodimer with calcineurin regulatory chain  
C;Function:  
A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to re  
C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei  
C;Keywords: alternative splicing; heterodimer; iron; metalloprotein; phosphoprotein; pho  
F;1-524/Product: protein phosphatase 3-beta catalytic chain splice form 2 #status predic  
F;1-456,467-524/Product: protein phosphatase 3-beta catalytic chain splice form 3 #statu  
F;65-337/Domain: phosphoprotein phosphatase homology <PPP>  
F;93-161/Domain: phosphoesterase core homology <P>  
F;93,161/Binding site: iron (Asp, His, Asp) #status predicted  
F;127,159,208,290/Binding site: zinc (Asp, Asn, His, His) #status predicted  
F;130,160,320/Active site: Asp, His, Tyr #status predicted  
F;131,263/Binding site: substrate phosphate (Arg) #status predicted  
F;420/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 87.0%; Score 2392.5; DB 1; Length 524;  
Best Local Similarity 96.0%; Pred. No. 7.5e-176;  
Matches 455; Conservative 0; Mismatches 0; Indels 19; Gaps 2;  
Qy 1 MAAPERARAPPPPPPPPPGADRVVKAVPPFPPTHLRTSEVFDLGGI PRVDVLKNHLV 60  
Db 1 MAAPERARAPPPPPPPPPGADRVVKAVPPFPPTHLRTSEVFDLGGI PRVDVLKNHLV 60  
Qy 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANT 120  
Db 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANT 120  
Qy 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 180  
Db 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 161

Qy 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 180  
Db 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 161  
Qy 181 CRHLTEYFTFKQCKIKYSERVYEACMEAFDSPLAALLNQQLFCLVHGGLSPEIHTLDDI 240  
Db 162 CRHLTEYFTFKQCKIKYSERVYEACMEAFDSPLAALLNQQLFCLVHGGLSPEIHTLDDI 221  
Qy 241 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQHFSHTVRGCSYFNYPAVCEFLQNN 300  
Db 222 RRLDRFKPEPPAFGPMCDLLWSDPSEDFGNEKSEQHFSHTVRGCSYFNYPAVCEFLQNN 281  
Qy 301 NLLSIIRAHEAQDAGYMYRKSQTTGPPSLITIFSAPNYLDVYNNKAALVLYENNVNIR 360  
Db 282 NLLSIIRAHEAQDAGYMYRKSQTTGPPSLITIFSAPNYLDVYNNKAALVLYENNVNIR 341  
Qy 361 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 420  
Db 342 QFNCSPPHYWLPNFMDFVFTWSLPPFVGEKVTMLVNVLSICSDDELMTEGEDQFDGSAAR 401  
Qy 421 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQ 474  
Db 402 KEIIRNKIRAIGKMARVSVLRRESESVLTILKGLTPTGMLPSGVLGGRTQLQ 455

RESULT 3  
A33794  
phosphoprotein phosphatase (EC 3.1.3.16) 3-beta catalytic chain - rat  
N;Alternate names: calcineurin catalytic chain; calcineurin chain A-beta; protein phosph  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 16-Aug-2004  
C;Accession: A33794; I36491  
R;Kuno, T.; Takeda, T.; Hirai, M.; Ito, A.; Mukai, H.; Tanaka, C.  
Biochem. Biophys. Res. Commun. 165, 1352-1358, 1989  
A;Title: Evidence for a second isoform of the catalytic subunit of calmodulin-dependent  
A;Reference number: A33794; MUID:90121248; PMID:2558657  
A;Accession: A33794  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-525 <KUN>  
A;Cross-references: UNIPROT:P20651; GB:M31809; NID:g203228; PIDN:AAA40848.1; PID:g203229  
R;Madzinski, B.E.; Heasley, L.E.; Johnson, G.L.  
J. Biol. Chem. 265, 21504-21508, 1990  
A;Title: Multiplicity of protein serine-threonine phosphatases in PC12 pheochromocytoma  
A;Reference number: A36491; MUID:91072341; PMID:2174876  
A;Accession: I36491  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 245-315 <WAD>  
A;Cross-references: GB:M58441; NID:g206308; PIDN:AAA1915.1; PID:g206309; GB:J05720  
C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase  
F;65-337/Domain: phosphoprotein phosphatase homology <PPP>  
F;93-161/Domain: phosphoesterase core homology <P>  
F;421/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 86.2%; Score 2370; DB 2; Length 525;  
Best Local Similarity 95.4%; Pred. No. 4e-174;  
Matches 453; Conservative 1; Mismatches 1; Indels 20; Gaps 3;  
Qy 1 MAAPERARAPPPPPPPPPGADRVVKAVPPFPPTHLRTSEVFDLGGI PRVDVLKNHLV 60  
Db 1 MAAPERARAPPPPPPPPPGADRVVKAVPPFPPTHLRTSEVFDLGGI PRVDVLKNHLV 60  
Qy 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANT 120  
Db 61 KEGRVDEIARLIINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANT 120  
Qy 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 180  
Db 121 RYFLGLGYVDRGYFSIEHVLGTEDISINPHNNINECVLYLWLKILYPSLTFLLLRGNHE 161

181 CRHLTEYFTFKQCKIKYISERVYACMEAFDLSPLAALLNQOFLCVHGLSPREIHTLDDI 240  
162 CRHLTEYFTFKQCKIKYISERVYACMEAFDLSPLAALLNQOFLCVHGLSPREIHTLDDI 221  
241 RRLDRFKPPAFGPMCDLLNSDPSEDFGNEKSQEHFSHNTVRGCSYFYNYPAVCEFLQNN 300  
222 RRLDRFKPPAFGPMCDLLNSDPSEDFGNEKSQEHFSHNTVRGCSYFYNYPAVCEFLQNN 281  
301 NLLSIIIRAHEAQAQAGYRMYRSQTTGPPSLITIFSAPNYLDVYNNKAALVKYENNVNMR 360  
282 NLLSIIIRAHEAQAQAGYRMYRSQTTGPPSLITIFSAPNYLDVYNNKAALVKYENNVNMR 341  
361 QFNCSPHYWLPNFMVDVFTWSLPFVGEKVTEMLNVNLSICSDDELMTEGEDQFD-GSAAA 419  
342 QFNCSPHYWLPNFMVDVFTWSLPFVGEKVTEMLNVNLSICSDDELMTEGEDQFDVGSAAA 401  
420 RKEIIRNKIRAIQKMARVFSVLRSESVLTGKLTPTGMLPSGVLAGGRQTLOS 474  
402 RKEIIRNKIRAIQKMARVFSVLRSESVLTGKLTPTGMLPSGVLAGGRQTLOS 456

RESULT 4  
JT0976  
Phosphoprotein phosphatase (EC 3.1.3.16) 3-alpha catalytic chain - mouse (fragment)  
N:Alternate names: calcineurin catalytic chain; calcineurin chain A; protein phosphatase  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JT0976; B45110  
R:Giri, P.R.; Higuchi, S.; Kincaid, R.L.  
Biochim. Biophys. Res. Commun. 181, 252-258, 1991  
A:Title: Chromosomal mapping of the human genes for the calmodulin-dependent protein phosphatase  
A:Reference number: JT0976; MUID:92068200; PMID:1659808  
A:Accession: JT0976  
A:Molecule type: mRNA  
A:Residues: 1-515 <GR>  
A:Cross-references: UNIPROT:P48453; GB:M81483; NID:g192537; PIDN:AAA37411.1; PID:g192538  
A:Experimental source: thymocyte  
R:Gaestel, M.; Benndorf, R.; Hayess, K.; Priemer, E.; Engel, K.  
J. Biol. Chem. 267, 21607-21611, 1992  
A:Title: Dephosphorylation of the small heat shock protein hsp25 by calcium/calmodulin-dependent protein kinase II  
A:Reference number: A45110; MUID:93016109; PMID:1328240  
A:Accession: B45110  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 310-406 <GAE>  
A:Experimental source: Ehrlich ascites tumor cells  
A:Note: sequence extracted from NCBI Backbone (NCBIP:116730)  
C:Comment: Multiple catalytic subunits of the Ca2+ and calmodulin (CaM)-dependent protein kinase II.  
C:Genetics:  
A:Map position: 10  
C:Superfamily: calcineurin catalytic chain; phosphoesterase core homology; phosphoprotein  
C:Keywords: calmodulin binding; phosphoprotein; phosphoric monoester hydrolase  
F:55-327/Domain: phosphoprotein phosphatase homology <PPP>  
F:83-151/Domain: phosphoesterase core homology <PEC>  
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #status predicted

Query Match 84.4%; Score 2321; DB 2; Length 515;  
Best Local Similarity 95.3%; Pred. No. 2.3e-170;  
Matches 443; Conservative 1; Mismatches 1; Indels 20; Gaps 3;

11 PPPPPPPPPGADRVKAVKVPFPPHRLTSEVFDLGIPRVDLKHLVKEGRVDEIA 70  
1 PPPPPPPPPGADRVKAVKVPFPPHRLTSEVFDMDGIPRVDLKHLVKEGRVDEIA 60  
71 LRIINEGAAILRREKTMIEVAPITVCQDINGQFPDLMKLFVGGSPANTRYLFLGDYVD 130  
61 LRIINEGAAILRREKTMIEVAPITVCQDINGQFPDLMKLFVGGSPANTRYLFLGDYVD 120  
131 RGYPSIEHVLGTEDISINPHNNIECVLYLVNLIKLYPSTLFLIIRGNHCECHLTYEYTF 190  
121 RGYPSI-----ECVLYLVNLIKLYPSTLFL-LIRGNHCECHLTYEYTF 161

191 KQECKIKYISERVYACMEAFDLSPLAALLNQOFLCVHGLSPREIHTLDDIRRLDRFKPSP 250  
162 KQECKIKYISERVYACMEAFDLSPLAALLNQOFLCVHGLSPREIHTLDDIRRLDRFKPSP 221  
251 AFGPMCDLLNSDPSEDFGNEKSQEHFSHNTVRGCSYFYNYPAVCEFLQNNLLSIIIRAHE 310  
222 AFGPMCDLLNSDPSEDFGNEKSQEHFSHNTVRGCSYFYNYPAVCEFLQNNLLSIIIRAHE 281  
311 AQDAGYRMYRSQTTGPPSLITIFSAPNYLDVYNNKAALVKYENNVNMRQFNCSPHYW 370  
282 AQDAGYRMYRSQTTGPPSLITIFSAPNYLDVYNNKAALVKYENNVNMRQFNCSPHYW 341  
371 LPNFMVDVFTWSLPFVGEKVTEMLNVNLSICSDDELMTEGEDQFD-GSAAARKKIIRNKIR 429  
342 LPNFMVDVFTWSLPFVGEKVTEMLNVNLSICSDDELMTEGEDQFDVGSAAARKKIIRNKIR 401  
430 AIGKMARVFSVLRSESVLTGKLTPTGMLPSGVLAGGRQTLOS 474  
402 AIGKMARVFSVLRSESVLTGKLTPTGMLPSGVLAGGRQTLOS 446

RESULT 5  
S35067  
Phosphoprotein phosphatase (EC 3.1.3.16) 3-alpha catalytic chain [similarity] - human  
N:Alternate names: calcineurin alpha chain A; calcineurin catalytic chain; protein phosphatase  
C:Species: Homo sapiens (man)  
C:Date: 10-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-2004  
C:Accession: S35067; B42232; T48685  
R:Muramatsu, T.; Kincaid, R.L.  
Biochim. Biophys. Acta 1178, 117-120, 1993  
A:Title: Molecular cloning of a full-length cDNA encoding the catalytic subunit of human phosphatase  
A:Reference number: S35067; MUID:93320118; PMID:8392375  
A:Accession: S35067  
A:Molecule type: mRNA  
A:Residues: 1-521 <MR>  
A:Cross-references: UNIPROT:Q08209; GB:L14778; NID:g306476; PIDN:AAA02631.1; PID:g306477  
R:Kincaid, R.L.; Giri, P.R.; Higuchi, S.; Tamura, J.; Dixon, S.C.; Marietta, C.A.; Amore, J.  
J. Biol. Chem. 265, 11312-11319, 1990  
A:Title: Cloning and characterization of molecular isoforms of the catalytic subunit of phosphatase  
A:Reference number: A42232; MUID:90293081; PMID:2162844  
A:Accession: B42232  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 269-521 <KIN>  
A:Cross-references: GB:J05480; NID:g179807; PIDN:AAA35634.1; PID:g179808  
R:Ansorge, W.; Winkler, U.; Mewes, H.W.; Weil, B.; Wiemann, S.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24534  
A:Accession: T48685  
A:Molecule type: mRNA  
A:Residues: 1-521 <AAA>  
A:Cross-references: ENBL:AL353950  
A:Experimental source: adult amygdala; clone DKFZp761L0516  
C:Genetics:  
A:Gene: GDB:PPP3CA; CALN; CCN1; CALNA; PPP2B  
A:Cross-references: GDB:118761; OMIM:114105  
A:Map position: 4c21-4q24pter-4qter  
A:Note: DKFZp761L0516.1  
C:Complex: heterodimer with calcineurin regulatory chain  
C:Function:  
A:Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to release phosphate  
C:Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotein  
C:Keywords: heterodimer; iron; metalloprotein; phosphoprotein; phosphoric monoester hydrolase  
F:56-328/Domain: phosphoprotein phosphatase homology <PPP>  
F:84-152/Domain: phosphoesterase core homology <PEC>  
F:90-92.118/Binding site: iron (Asp, His, Asp) #status predicted  
F:118,150,199,281/Binding site: zinc (Asp, Asn, His, His) #status predicted  
F:121,151,311/Active site: Asp, His, Tyr #status predicted  
F:122,254/Binding site: substrate phosphate (Arg) #status predicted  
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #status predicted

Query Match 74.8%; Score 2057.5; DB 1; Length 521;  
Best Local Similarity 83.6%; Pred. No. 4e-150;





Proc. Natl. Acad. Sci. U.S.A. 85, 8983-8987, 1988  
A>Title: Characterization of a cDNA clone encoding the calmodulin-binding domain of mouse  
A/Reference number: A31257; MUID:89057863; PMID:2848250  
A/Accession: A31257  
A/Molecule type: mRNA  
A/Residues: 215-521 <X12>  
A/Cross-references: GB:J04134; NID:g192656; PIDN:AAA37432.1; PID:g192657  
A/Note: bovine calcineurin tryptic fragments were also sequenced  
R/Gastel, M.; Benndorf, R.; Hayess, K.; Priemer, E.; Engel, K.  
J. Biol. Chem. 267, 21607-21611, 1992  
A>Title: Dephosphorylation of the small heat shock protein hsp25 by calcium/calmodulin-  
A/Reference number: A45110; MUID:93016109; PMID:1328240  
A/Accession: A45110  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 311-406 <GAE>  
A/Experimental source: Ehrlich ascites tumor cells  
A/Note: sequence extracted from NCB1 backbone (NCBIP:116727)  
R/Truman, D.A.; Pai, S.Y.; Burakoff, S.J.; Blierer, B.E.  
Mol. Cell. Biol. 15, 3857-3863, 1995  
A>Title: Characterization of a mutant calcineurin A alpha gene expressed by EL4 lymphoma  
A/Reference number: I57562; MUID:95311985; PMID:7791792  
A/Accession: I57562  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 467-476, 'N', 478-491 <RES>  
A/Cross-references: GB:S78668; NID:g1042087; PIDN:AAB34675.1; PID:g1042088  
A/Note: this mutation changes an evolutionarily conserved aspartic acid to asparagine wh  
C/Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei  
C/Keywords: calmodulin binding; phosphoprotein; phosphoric monoester hydrolase  
F:156-328/Domain: phosphoprotein phosphatase homology <PPP>  
F:184-152/Domain: phosphoesterase core homology <PEC>  
F:391-414/Region: calmodulin binding #status predicted  
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 74.7%; Score 2054.5; DB 2; Length 521;  
Best Local Similarity 83.4%; Pred. No. 6.9e-150;  
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;  
QY 13 PPPPPPPGADRVVKA VPPFPPTHRLTSEEVFDLDGI PRVDVLKHLVKEGRVDEIALR 72  
DB 4 PKAIDPKLSTTDRVVKA VPPFPSSHRLTAKEVFDNDGKPRVDILKAHLMKGRLEESVALR 63  
QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 132  
DB 64 IITEGASILRQEKNLDDIDAPVTTCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 123  
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVILKILYPSLTLFLLLRGNHCHRLTEYFTPKQ 192  
DB 124 YFSI-----ECVLYLWALKILYPKTLF--LLRGNHCHRLTEYFTPKQ 164  
QY 193 ECKIKYSERVYEAQMEAFDSLPLAALNQOFLCVHGGLSPEIHTLDDIRRLDRFKPEPPAF 252  
DB 165 ECKIKYSERVYDQCMDFCDPLAALMNQOFLCVHGGLSPEINTLDDIRKLDLRFKPEPPAY 224  
QY 253 GPMCDLLWSDFEDFGNEKSGHEFHSNTRVRCGSFYFYNYPVACEFLQNNLLSIIIRAHAQ 312  
DB 225 GPMCDLLWSDFLEDFGNEKTQEHFTHNTRVRCGSFYFYSYPVAVCDFLQNNLLSIIIRAHAQ 284  
QY 313 DAGYRMYSKQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPPHYWLP 372  
DB 285 DAGYRMYSKQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPPHYWLP 344  
QY 373 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG--SAAARKEIIRNKIRAI 431  
DB 345 NFMDFVFTWSLFPVGEKVTMELVNVNINICSDDELGSE--BDGFDGATAAARKEVIRNKIRAI 403  
QY 432 GKMARVFSVLRSESVLTLKGLTPTGMLPSGVLAGGQTLQS 474  
DB 404 GKMARVFSVLRSESVLTLKGLTPTGMLPSGVLAGGQTLQS 446

RESULT 8

A33264  
phosphoprotein phosphatase (EC 3.1.3.16) 3-alpha catalytic chain - rat  
N/Alternate names: calcineurin catalytic chain; calcineurin chain A-alpha; protein phosph  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 21-Feb-1990 #sequence revision 21-Feb-1990 #text\_change 16-Aug-2004  
C/Accession: A33264; S27349; H36491  
R/Rito, A.; Hashimoto, T.; Hirai, M.; Takeda, T.; Shuntoh, H.; Kuno, T.; Tanaka, C.  
Biochem. Biophys. Res. Commun. 163, 1492-1497, 1989  
A>Title: The complete primary structure of calcineurin A, a calmodulin binding protein h  
A/Reference number: A33264; MUID:89192066; PMID:2551293  
A/Accession: A33264  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-521 <ITO>  
A/Cross-references: UNIPROT:P20652; GB:M29275; NID:g203494; PIDN:AAA40940.1; PID:g203495  
R/Chang, C.D.; Takeda, T.; Mukai, H.; Shuntoh, H.; Kuno, T.; Tanaka, C.  
Biochem. J. 288, 801-805, 1992  
A>Title: Molecular cloning and characterization of the promoter region of the calcineuri  
A/Reference number: S27349; MUID:93111954; PMID:1335233  
A/Accession: S27349  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-19 <CHA>  
A/Cross-references: EMBL:D10480; NID:g220679; PIDN:BAA01283.1; PID:g220680  
R/Wadzinaki, B.E.; Heasley, L.E.; Johnson, G.L.  
J. Biol. Chem. 265, 21504-21508, 1990  
A>Title: Multiplicity of protein serine-threonine phosphatases in PC12 pheochromocytoma  
A/Reference number: A36491; MUID:91072341; PMID:2174876  
A/Accession: H36491  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 236-306 <WAD>  
A/Cross-references: GB:M58440; NID:g206306; PIDN:AAA41914.1; PID:g206307; GB:J05720  
C/Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotei  
C/Keywords: phosphoprotein; phosphoric monoester hydrolase  
F:156-328/Domain: phosphoprotein phosphatase homology <PPP>  
F:184-152/Domain: phosphoesterase core homology <PEC>  
F:411/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 74.7%; Score 2054.5; DB 2; Length 521;  
Best Local Similarity 83.4%; Pred. No. 6.9e-150;  
Matches 386; Conservative 35; Mismatches 21; Indels 21; Gaps 4;  
QY 13 PPPPPPPGADRVVKA VPPFPPTHRLTSEEVFDLDGI PRVDVLKHLVKEGRVDEIALR 72  
DB 4 PKAIDPKLSTTDRVVKA VPPFPSSHRLTAKEVFDNDGKPRVDILKAHLMKGRLEESVALR 63  
QY 73 IINEGAAILRREKTMIEVEAPITVCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 132  
DB 64 IITEGASILRQEKNLDDIDAPVTTCGDIHGQFFDLMLKLFVGGSPANTRYILFLGDYVDRG 123  
QY 133 YFSIEHVLGTEDISINPHNNINECVLYLWVILKILYPSLTLFLLLRGNHCHRLTEYFTPKQ 192  
DB 124 YFSI-----ECVLYLWALKILYPKTLF--LLRGNHCHRLTEYFTPKQ 164  
QY 193 ECKIKYSERVYEAQMEAFDSLPLAALNQOFLCVHGGLSPEIHTLDDIRRLDRFKPEPPAF 252  
DB 165 ECKIKYSERVYDQCMDFCDPLAALMNQOFLCVHGGLSPEINTLDDIRKLDLRFKPEPPAY 224  
QY 253 GPMCDLLWSDFEDFGNEKSGHEFHSNTRVRCGSFYFYNYPVACEFLQNNLLSIIIRAHAQ 312  
DB 225 GPMCDLLWSDFLEDFGNEKTQEHFTHNTRVRCGSFYFYSYPVAVCDFLQNNLLSIIIRAHAQ 284  
QY 313 DAGYRMYSKQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPPHYWLP 372  
DB 285 DAGYRMYSKQTTGPPSLITIFSAAPNYLDVYNNKAAVLKYENNVNINIQFNCSPPHYWLP 344  
QY 373 NFMDFVFTWSLFPVGEKVTMELVNVLSICSDDELMTGEDQFDG--SAAARKEIIRNKIRAI 431  
DB 345 NFMDFVFTWSLFPVGEKVTMELVNVNINICSDDELGSE--BDGFDGATAAARKEVIRNKIRAI 403  
QY 432 GKMARVFSVLRSESVLTLKGLTPTGMLPSGVLAGGQTLQS 474



Db 404 GKMARVSVLREESESVLTLLKGLTPTGMLPSGVLSGGKQTLLQS 446

RESULT 9

JC1283

phosphoprotein phosphatase (EC 3.1.3.16) 3-gamma catalytic chain - human

N;Alternate names: calcineurin catalytic chain; calcineurin chain A; protein phosphatase

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-2004

C;Accession: JCI1283

R;Muramatsu, T.; Kincaid, R.L.

Biochem. Biophys. Res. Commun. 188, 265-271, 1992

A;Title: Molecular cloning and chromosomal mapping of the testis-spec

A;Reference number: JCI1283; MUID:93038669; PMID:1339277

A;Accession: JCI1283

A;Molecule type: mRNA

A;Residues: 1-502 <MUR>

A;Cross-references: UNIPROT:P48454; GB:S46622; NID:g258000; PIDN:AAB23769.1; PID:g258001

A;Experimental source: testis

C;Genetics:

A;Gene: GDB:PPP3CC

A;Cross-references: GDB:I36027; OMIM:114107

A;Map position: 8pter-8qter

C;Complex: heterodimer with calcineurin regulatory chain

C;Function:

A;Description: catalyzes hydrolysis of peptidyl-phosphoserine or -phosphothreonine to re

A;Note: this isoform is testis specific and is associated with sperm flagellar motility

C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotein

C;Keywords: heterodimer; iron; metalloprotein; phosphoprotein; phosphoric monoester hyd

F;52-324/Domain: phosphoprotein phosphatase homology <PPP>

F;80-148/Domain: phosphoesterase core homology <PEC>

F;86,88,114/Binding site: iron (Asp, His, Asp) #status predicted

F;114,146,195,277/Binding site: zinc (Asp, Asn, His, His) #status predicted

F;117,147,307/Active site: Asp, His, Tyr #status predicted

F;118,250/Binding site: substrate phosphate (Arg) #status predicted

F;405/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #stat

Query Match 72.2%; Score 1985; DB 1; Length 502;

Best Local Similarity 82.3%; Pred. No. 1.4e-144;

Matches 371; Conservative 40; Mismatches 18; Indels 22; Gaps 4;

Qy 24 DRVVKAVPPPTPRLTSEEVFDLGGIPRDVVLKNHLVKEGRVDEEIALRIINEGAAILRR 83

Db 12 DRVVKAVPPPTPRLTSEEVFDLGGIPRDVVLKNHLVKEGRVDEEIALRIINEGAAILRR 70

Qy 84 EKTWIEVAPITVCGDIHGQFFDLMLKLFVGGSPANTRYFLGDIYVDRGYFSIEHVLGTE 143

Db 71 EKTWIEVAPITVCGDIHGQFFDLMLKLFVGGSPANTRYFLGDIYVDRGYFSI----- 123

Qy 144 DISINPHNINECVLYLWLVKILYPSITFLLRGNHCHRLTETFTFKQECRIKYSERVY 203

Db 124 -----ECVLYLWLSLKINHPTLFL--LLRGNHCHRLTETFTFKQECRIKYSERVY 171

Qy 204 EACWEAFDSLPALALNQOFLCVHGGSPETITLDDIRLRDRKEPPAFGPMCDLLMSDP 263

Db 172 DACWETFDCLPLAALLNQOFLCVHGGSPETITLDDIRLRDRKEPPAFGPMCDLLMSDP 231

Qy 264 SEDFGNKSQBFHSNTVRGCSYFYNPVAVCEFLQNNLLSIIIRAHEAQDAGYRMVRSQ 323

Db 232 SEDYGNKTLTLEHYTHNTVRGCSYFYNPVAVCEFLQNNLLSIIIRAHEAQDAGYRMVRSQ 291

Qy 324 TTGFPSSLITFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTWSLP 383

Db 292 ATGFPSSLITFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTWSLP 351

Qy 384 FVGEKVTMLVNVLSICSDDELMTGEGDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE 443

Db 352 FVGEKVTMLVNVLSICSDDELMTGEGDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE 409

Qy 444 ESESVLTLLKGLTPTGMLPSGVLAGGRTLLQS 474

Db 410 ESESVLTLLKGLTPTGMLPSGVLAGGRTLLQS 440

RESULT 10

A38193

phosphoprotein phosphatase (EC 3.1.3.16) 3-gamma catalytic chain - mouse

N;Alternate names: calcineurin catalytic chain; calcineurin chain A; nonneural calmodulin

C;Species: Mus musculus (house mouse)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-2004

C;Accession: A38193

R;Muramatsu, T.; Giri, P.R.; Higuchi, S.; Kincaid, R.L.

Proc. Natl. Acad. Sci. U.S.A. 89, 529-533, 1992

A;Title: Molecular cloning of a calmodulin-dependent phosphatase from murine testis: ide

A;Reference number: A38193; MUID:92115694; PMID:1309945

A;Accession: A38193

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-513 <MUR>

A;Cross-references: UNIPROT:P48455; GB:M81475; NID:g200465; PIDN:AAA39968.1; PID:g200466

A;Experimental source: testis

A;Note: sequence extracted from NCBI backbone (NCBIN:75959, NCBI:P:75960)

C;Function:

A;Description: catalyzes the hydrolysis of peptidyl-phosphoserine and -phosphothreonine

A;Note: this isoform is testis specific and is associated with sperm flagellar motility

C;Superfamily: Calcineurin catalytic chain; phosphoesterase core homology; phosphoprotein

C;Keywords: calmodulin binding; phosphoric monoester hydrolase; testis

F;52-324/Domain: phosphoprotein phosphatase homology <PPP>

F;80-148/Domain: phosphoesterase core homology <PEC>

Query Match 69.8%; Score 1919.5; DB 2; Length 513;

Best Local Similarity 78.9%; Pred. No. 1.6e-139;

Matches 356; Conservative 47; Mismatches 25; Indels 23; Gaps 4;

Qy 24 DRVVKAVPPPTPRLTSEEVFDLGGIPRDVVLKNHLVKEGRVDEEIALRIINEGAAILRR 83

Db 12 ERVVKAVPPPTPRLTSEEVFDLGGIPRDVVLKNHLVKEGRVDEEIALRIINEGAAILRR 70

Qy 84 EKTWIEVAPITVCGDIHGQFFDLMLKLFVGGSPANTRYFLGDIYVDRGYFSIEHVLGTE 143

Db 71 EKTWIEVAPITVCGDIHGQFFDLMLKLFVGGSPANTRYFLGDIYVDRGYFSI----- 123

Qy 144 DISINPHNINECVLYLWLVKILYPSITFLLRGNHCHRLTETFTFKQECRIKYSERVY 203

Db 124 -----ECVLYLWLSLKINHPTLFL--LLRGNHCHRLTETFTFKQECRIKYSERVY 171

Qy 204 EACWEAFDSLPALALNQOFLCVHGGSPETITLDDIRLRDRKEPPAFGPMCDLLMSDP 263

Db 172 DACWETFDCLPLAALLNQOFLCVHGGSPETITLDDIRLRDRKEPPAFGPMCDLLMSDP 231

Qy 264 SEDFGNKSQBFHSNTVRGCSYFYNPVAVCEFLQNNLLSIIIRAHEAQDAGYRMVRSQ 323

Db 232 LEDYGSSEKTLTLEHYTHNTVRGCSYFYNPVAVCEFLQNNLLSIIIRAHEAQDAGYRMVRSQ 291

Qy 324 TTGFPSSLITFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTWSLP 383

Db 292 ATGFPSSLITFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPPHYLWLPNFMDFVFTWSLP 351

Qy 384 FVGEKVTMLVNVLSICSDDELMTGEGDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE 443

Db 352 FVGEKVTMLVNVLSICSDDELMTGEGDQFDGSAARKEIIRNKIRAIQKMARVFSVLRE 408

Qy 444 ESESVLTLLKGLTPTGMLPSGVLAGGRTLLQS 474

Db 409 ESESVLTLLKGLTPTGMLPSGVLAGGRTLLQS 439

RESULT 11

JC7241

phosphoprotein phosphatase (EC 3.1.3.16), calcineurin catalytic chain [similarity] - sca

N;Alternate names: Ca2+/calmodulin-dependent phosphoprotein phosphatase catalytic subunit

C;Species: Patinopecten yessoensis (Yesso scallop)

C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 16-Aug-2004

C;Accession: JC7241; PC7069

R;Uryu, M.; Nakatomi, A.; Watanabe, M.; Hatause, R.; Yazawa, M.

J. Biochem. 127, 739-746, 2000







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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 14:04:18 ; Search time 58.073 Seconds  
(without alignments)  
1132.183 Million cell updates/sec

Title: US-09-435-257D-35  
Perfect score: 875  
Sequence: 1 MGNEASYPLEMCSHFDADEI.....BEFCVAVGGLDIHKVMVDV 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_16Dec04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	875	100.0	170	2	Aaw64200 Human cal
2	875	100.0	170	3	Aab09978 Human HCN
3	875	100.0	170	8	ADI27357 Human cal
4	870	99.4	169	7	Ades5926 Rat Prote
5	870	99.4	169	7	Ades5928 Human Pro
6	767	87.7	170	4	Abb60493 Drosophil
7	739	84.5	162	4	Abb65554 Drosophil
8	738	84.3	170	4	Aaol14411 Calcineur
9	738	84.3	173	4	Aab64410 Amino aci
10	738	84.3	173	6	Ada55632 Human pro
11	738	84.3	187	4	Aau87327 Novel cen
12	738	84.3	187	8	Adi54642 Novel hum
13	738	84.3	189	4	Aam95239 Human rep
14	738	84.3	189	4	Aam43639 Human pol
15	738	84.3	189	4	Aam43564 Human pol
16	738	84.3	189	4	Aau19951 Novel hum
17	738	84.3	189	4	Abb95936 Human tes
18	738	84.3	189	4	Aau87615 Novel cen
19	738	84.3	189	8	Adi54930 Novel hum
20	738	84.3	189	8	Adm24660 Human PRO
21	738	84.3	189	8	Adm24585 Human PRO
22	733	83.8	170	3	Aab09977 Human CNB
23	501	57.3	197	8	AdS24073 Bacterial
24	496	56.7	175	2	Aay00881 Calcineur
25	496	56.7	175	8	AdS43790 Bacterial

ALIGNMENTS

RESULT 1

AAW64200  
ID AAW64200 standard; protein; 170 AA.  
XX  
AC AAW64200;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Human calcineurin.  
XX  
KW Calcineurin; interferon receptor 1 binding protein; IR1B1; human.  
XX  
OS Homo sapiens.  
XX  
PN WO9831796-A1.  
XX  
PD 23-JUL-1998.  
XX  
PF 15-JAN-1998; 98WO-US000671.  
XX  
PR 15-JAN-1997; 97US-0035636P.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (MCIN/) MCINNIS P A.  
XX  
Revel M, Abramovitch C, Chebath JE;  
XX  
WPI, 1998-414096/35.  
XX  
New isolated interferon receptor binding proteins - used to develop products for modulating sensitivity to interferon, e.g. in the treatment of tumours or for prolonging graft survival.  
XX  
Example 2; Page 35-36; 64pp; English.  
XX  
This polypeptide comprises the human calcium-binding protein, calcineurin -beta. A novel interferon receptor binding protein, IR1B1 (see AAW64199), of the invention shows marked homology, e.g. calcium binding sites (E-P handles), to calcineurin-beta; amino acid residues 50-171 show 59.8% similarity and 32.5% identity. IR1B1 polypeptides and polynucleotides can be used to develop products for modulating sensitivity to interferon, e.g. in cancer therapy and for prolonging graft survival  
XX  
SQ Sequence 170 AA;

Query Match 100.0%; Score 875; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 2.8e-83;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





Db 1 MNEASYPLEMCSHFDADAEIKELGRFKKLDLDNSSLVSVEEFMSLPELQQNPLVQRVID 60  
Qy 61 IFDTDNGEVDPFKEFIEGVVSQSVKGDKEQKLPFAFRIYDMDKDGYISNGELFQVLKMWV 120  
Db 61 IFDTDNGEVDPFKEFIEGVVSQSVKGDKEQKLPFAFRIYDMDKDGYISNGELFQVLKMWV 120  
Qy 121 GNNLKDQTOLQIIVDKTIINADKDGGRISFEFCAVVGGLDIHKMWVDV 170  
Db 121 GNNLKDQTOLQIIVDKTIINADKDGGRISFEFCAVVGGLDIHKMWVDV 170

RESULT 4  
ADES5926  
ID ADE55926 standard; protein; 169 AA.  
XX  
AC ADE55926;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein P06705, SEQ ID NO 1760.  
XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
FF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
FA (GEHO ) GEN HOSPITAL CORP.  
FA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P06705.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 169 AA;  
Query Match 99.4%; Score 870; DB 7; Length 169;  
Best Local Similarity 100.0%; Pred. No. 9.2e-83;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GNEASYPLEMCSHFDADAEIKELGRFKKLDLDNSSLVSVEEFMSLPELQQNPLVQRVID 61  
Db 1 GNEASYPLEMCSHFDADAEIKELGRFKKLDLDNSSLVSVEEFMSLPELQQNPLVQRVID 60  
Qy 62 FDTDNGEVDPFKEFIEGVVSQSVKGDKEQKLPFAFRIYDMDKDGYISNGELFQVLKMWV 121  
Db 61 FDTDNGEVDPFKEFIEGVVSQSVKGDKEQKLPFAFRIYDMDKDGYISNGELFQVLKMWV 120  
Qy 122 NNLKDTOLQIIVDKTIINADKDGGRISFEFCAVVGGLDIHKMWVDV 170  
Db 121 NNLKDTOLQIIVDKTIINADKDGGRISFEFCAVVGGLDIHKMWVDV 169  
RESULT 5  
ADES5928  
ID ADE55928 standard; protein; 169 AA.  
XX  
AC ADE55928;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P06705, SEQ ID NO 1762.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
FA (GEHO ) GEN HOSPITAL CORP.  
FA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P06705.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 169 AA;  
 CC Query Match 99.4%; Score 870; DB 7; Length 169;  
 CC Best Local Similarity 100.0%; Pred. No. 9.2e-83;  
 CC Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVVEFMSLPQLQNPVQRVIDI 61  
 DB 1 GNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVVEFMSLPQLQNPVQRVIDI 60  
 QY 62 FDTGNGEVDPKFIEGVQSVKDGKQKLRFAFRFYDMDKGYISNGELFQVLKMWVG 121  
 DB 61 FDTGNGEVDPKFIEGVQSVKDGKQKLRFAFRFYDMDKGYISNGELFQVLKMWVG 120  
 QY 122 NNLKDTLQQLVDTKIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 170  
 DB 121 NNLKDTLQQLVDTKIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 169

RESULT 6  
 ABB60493  
 ID ABB60493 standard; protein; 170 AA.  
 XX AC ABB60493;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 8271.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical.  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL04596.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions.  
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell interactions.  
 XX PS Disclosure; SEQ ID NO 8271; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 170 AA;

CC Query Match 87.7%; Score 767; DB 4; Length 170;  
 CC Best Local Similarity 85.9%; Pred. No. 5.7e-72;  
 CC Matches 146; Conservative 13; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKLDLNSGSLSVVEFMSLPQLQNPVQRVID 60  
 DB 1 MGNETSLPMDMCSNFDADAERRLGKRFKLDLNSGALSIDEFMSLPQLQNPVQRVID 60  
 QY 61 IFDTGNGEVDPKFIEGVQSVKDGKQKLRFAFRFYDMDKGYISNGELFQVLKMWV 120  
 DB 61 IFDADGNGEVDPKFIEGVQSVKDGKQKLRFAFRFYDMDKGYISNGELFQVLKMWV 120  
 QY 121 GNNLKDTLQQLVDTKIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 170  
 DB 121 GNNLKDTLQQLVDTKIINADKDGGRISPEEFCAVVGGLDIHKMWVDV 170

RESULT 7  
 ABB65554  
 ID ABB65554 standard; protein; 162 AA.  
 XX AC ABB65554;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 23454.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical.  
 XX OS Drosophila melanogaster.  
 XX PN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEKE ) PE CORP NY.  
 XX PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX DR WPI; 2001-656860/75.  
 XX DR N-PSDB; ABL09657.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

XX PS Disclosure; SEQ ID NO 23454; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

are useful for treating acute and chronic cardiac failure of different etiologies, myocardial infarction, cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension, cardiotoxicity, coronary heart disease, and as contraceptives. The polypeptides are also useful for identifying membrane bound soluble receptors. The polynucleotides are useful as a diagnostic reagent, for chromosome localization studies, and for tissue expression studies. The polypeptides and polynucleotides are also useful as vaccines for inducing an immunological response in mammals. The polypeptides and polynucleotides of the invention are also useful for configuring screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides and polynucleotides of the invention have cardiant, antiarrhythmic, antiinflammatory, hypotensive, and contraceptive activities, and can treat disorders by way of gene therapy

Sequence 170 AA;

Query Match 84.3%; Score 738; DB 4; Length 170;  
Best Local Similarity 84.7%; Pred. No. 6.2e-69;  
Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0

Qy 1 MGN EASYPLEMCSHFDADEIKLGRPFKLLDLDNGSLSVSEFMSLPQLQNPLVQRVID 60  
Db 1 MGN EASYPAEMCSHFNDDEIKLGRPFKLLDLDKSLSVSEFMSLPRLRHNPLVRRVID 60  
Qy 61 IFPTDNGEVDVDFEFIEGVQSFKGDKQKRLRFARIYDMDKGYISNGELFQVLKMMV 120  
Db 61 VFPTDGDGEVDVDFEFILGTSQFSVKGDDEQKLRFAFSIYDMDKGYISNGELFQVLKMMV 120  
Qy 121 GNNLKDTLOQLVDKTTIINADKDGGRISPEEPCAVVGGLDIHKQWVDV 170  
Db 121 GNNLTDWQLQQLVDKTTIILDKDGGKISPEEFSAVVRDLRDIHKKVLIV 170

RESULT 9  
AAB64410  
ID AAB64410 standard; protein; 173 AA.  
AC AAB64410;  
XX  
DT 22-MAR-2001 (first entry)  
XX  
DE Human; intracellular signalling molecule; INTRA; immunosuppressive;  
KW cytostatic; neuroprotective; nootropic; antiarteriosclerotic; cancer;  
KW antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;  
KW antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;  
KW cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;  
KW inflammatory disorder; Addison's disease; gastrointestinal disorder;  
KW neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;  
KW mental disorder; schizophrenia; anxiety.  
XX  
OS Homo sapiens.  
XX  
XX WO200077040-A2.  
XX  
XX 21-DEC-2000.  
XX  
XX 16-JUN-2000; 2000WO-US016636.  
XX  
XX 16-JUN-1999; 99US-0139566P.  
PR 17-AUG-1999; 99US-0149640P.  
PR 09-NOV-1999; 99US-0164417P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;  
PI Azimzai Y, Yang J, Reddy R, Lu DAM;  
XX  
XX WFI; 2001-025334/03.  
DR N-PSDB; AAF32679.  
XX

PT New human intracellular signaling molecules, useful for the diagnosis,  
 PT prevention and treatment of cell proliferative, autoimmune, inflammatory,  
 PT neurological, gastrointestinal, reproductive and developmental disorders.

XX Claim 5; Page 152; 192pp; English.

PS Sequences AAF32638 - AAF32689 represent cDNA encoding human intracellular  
 CC signalling molecules INTRAL - INTRAS2, represented in AB64369 -  
 CC AB64420. Modulators of the intracellular signalling molecules of the  
 CC invention exhibit immunosuppressive; cytostatic; neuroprotective;  
 CC neurotropic; antiarteriosclerotic; anti-inflammatory; anti-HIV; neuroleptic;  
 CC antibacterial; antifungal; antiviral; antiparasitic; antihelminthic; and  
 CC antiparkinsonian activity. INTRA polypeptides their agonists and  
 CC antagonists are useful for the treatment of a condition associated with  
 CC decreased or increased expression of functional INTRA. Disorders  
 CC associated with abnormal INTRA expression or activity include cell  
 CC proliferative disorders e.g. arteriosclerosis and cancers; autoimmune or  
 CC inflammatory disorders e.g. Addison's disease and acquired  
 CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,  
 CC protozoal and helminthic infections; gastrointestinal disorders e.g.  
 CC dysphagia and irritable bowel syndrome; neurological disorders e.g.  
 CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob  
 CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's  
 CC disorder. Antibodies immuno specific for the INTRA proteins may also be  
 CC useful in the diagnosis of the above disorders

XX Sequence 173 AA;

Query Match 84.3%; Score 738; DB 4; Length 173;  
 Best Local Similarity 84.7%; Pred. No. 6.3e-69;  
 Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGNEASYPLEMCSEHFDADDEIKRLGKRFKLLDNGSLSEVEEFMSLPQLQNPVLVQVRVID 60  
 Db 4 MGNEASYPAEKCSHFNDDEIKRLGRFRFKLLDNGSLSEVEEFMSLPQLRNPVLRVID 63  
 Qy 61 IFDTGNGEVDFKEFIEGVSQFSVKGDEQKLFAPRIYDMDKDGYISNGELFOVLKMWV 120  
 Db 64 VFDTGNGEVDFKEFIEGVSQFSVKGDEEQKLFAPRISYDMDKDGYISNGELFOVLKMWV 123  
 Qy 121 GNNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVVGGLDIHKKMWVVDV 170  
 Db 124 GNNLTWQLQQLVDKTIILDKDGGKISPEEFSVAVVRDLHKKLVLI 173

RESULT 10

ADA55632  
 ID ADA55632 standard; protein; 173 AA.

XX ADA55632;  
 XX  
 AC  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 XX Human protein, SEQ ID 3200.  
 DE  
 XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Neurotropic;  
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
 KW inflammatory disease; osteoporosis; neurological disease.

XX Homo sapiens.  
 OS  
 XX  
 XX  
 PN EP1293569-A2.  
 XX  
 PD 19-MAR-2003.  
 XX  
 XX 21-MAR-2002; 2002EP-00006586.  
 XX  
 XX 14-SEP-2001; 2001JP-00328381.  
 PR 24-JAN-2002; 2002US-0350435P.  
 XX  
 XX (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 PA  
 XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX WPI; 2003-395539/38.  
 DR N-PSDB; ADA53993.  
 DR

XX New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 PT which the gene is involved, or as target molecules for gene therapy.

XX Claim 14; SEQ ID NO 3200; 205pp; English.

XX The present invention relates to novel human secretory or membrane  
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA5433-  
 CC ADA54071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 173 AA;

Query Match 84.3%; Score 738; DB 6; Length 173;  
 Best Local Similarity 84.7%; Pred. No. 6.3e-69;  
 Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGNEASYPLEMCSEHFDADDEIKRLGKRFKLLDNGSLSEVEEFMSLPQLQNPVLVQVRVID 60  
 Db 4 MGNEASYPAEKCSHFNDDEIKRLGRFRFKLLDNGSLSEVEEFMSLPQLRNPVLRVID 63  
 Qy 61 IFDTGNGEVDFKEFIEGVSQFSVKGDEQKLFAPRIYDMDKDGYISNGELFOVLKMWV 120  
 Db 64 VFDTGNGEVDFKEFIEGVSQFSVKGDEEQKLFAPRISYDMDKDGYISNGELFOVLKMWV 123  
 Qy 121 GNNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVVGGLDIHKKMWVVDV 170  
 Db 124 GNNLTWQLQQLVDKTIILDKDGGKISPEEFSVAVVRDLHKKLVLI 173

RESULT 11

AAU87327  
 ID AAU87327 standard; protein; 187 AA.

XX AAU87327;  
 XX  
 AC  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 XX Novel central nervous system protein #237.  
 DE  
 XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
 KW myocardial infarction; wound healing; cell proliferation; skin aging;  
 KW food additive; food preservative; gene therapy.

XX Homo sapiens.  
 OS  
 XX  
 XX  
 PN WO200155318-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 17-JAN-2001; 2001WO-US001332.  
 XX  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234224P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236803P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
(HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-581633/65.  
XX N-PSDB; ABK43657.  
XX  
XX New isolated nucleic acid encoding a protein for diagnosing, preventing,  
XX treating or ameliorating medical conditions and used as food additives or  
XX preservatives.  
XX  
XX Claim 9; SEQ ID NO 845; 837pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
XX novel central nervous system protein. (I) and polypeptides (III) encoded

CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 84.3%; Score 738; DB 4; Length 187;

Best Local Similarity 84.7%; Pred. No. 7e-59;

Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGNEASYPLEMCSHFDADKRLGKRPFKLLDNLGSLSVSEFMSLPQLQNPVLQVRVID 60

Db 18 MGNEASYPACMSCHFDNDKRLGRFRFKLLDNLGSLSVSEFMSLPQLRHNPLVRVID 77

Qy 61 IFDTDNGEVDKFEFVGVSQFSVKGDKEQKLFAPRIYDMDKDGYISNGELFQVLKQMV 120

Db 78 VFDTDNGEVDKFEFLGTSQFSVKGBDEQKLFAPRIYDMDKDGYISNGELFQVLKQMV 137

Qy 121 GNNLKTQLQIQVDTKIINADKQDGRISFEFCVAVGGLDIHKMKVVDV 170

Db 138 GNNLTDWLQQLVDTKIILDKDGDGKISFEFSVAVRDLIHKKLIV 187

RESULT 12

ADIS4642

ID ADIS4642 standard; protein; 187 AA.

XX AC ADIS4642;

XX DT 22-APR-2004 (first entry)

XX DE Novel human protein seq id 845.

XX KW neuroprotective; neurotropic; antiparkinsonian; anticonvulsant;  
KW antidiabetic; antirheumatic; antiarthritic; dermatological;  
KW anti-inflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;  
KW anti-HIV; hepatotropic; virucide; antibacterial; fungicide;  
KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;  
KW cardiovascular; antiarteriosclerotic; antiarrhythmic; cardiac;  
KW nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;  
KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;  
KW amyotrophic lateral sclerosis; multiple sclerosis;  
KW immune system disorder; diabetes; rheumatoid arthritis;  
KW systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;  
KW inflammatory disorder; ischaemia-reperfusion injury;  
KW inflammatory bowel disease; Crohn's disease; infectious disease;  
KW HIV infection; hepatitis infection; bacterial infection;  
KW fungal infection; parasitic infection; muscular disorder;  
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;  
KW cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;  
KW renal disorder; acute glomerulonephritis; pyelonephritis;  
KW renal lithiasis; proliferative disorder; cancerous diseases; human.

XX Homo sapiens.

XX US2004018969-A1.

XX

PD 29-JAN-2004.  
XX 17-JAN-2001; 2001US-00764875.  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 11-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-022824P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 06-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
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PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234988P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
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PR 05-JAN-2001; 2001US-0259678P.

XX (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.

XX PI Rosen CA, Ruben SM, Barash SC;

XX WPI; 2004-122079/12.  
DR N-PSDB; ADI54044.  
XX  
PT New polypeptides and nucleic acid molecules, useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions e.g. neural disorders, reproductive disorders or infectious diseases.  
PT  
XX  
PS Claim 11; SEQ ID NO 845; 413pp; English.  
XX  
CC The invention describes an isolated polypeptide comprising an amino acid sequence at least 90% identical to: a polypeptide fragment, domain, epitope, or full-length protein of any one of 607 amino acid sequences (I) described in the specification; a polypeptide fragment of (I), or the encoded sequence contained in (II), having biological activity; or a variant, allelic variant, or a species homologue of (I). The polypeptides and nucleic acid molecules are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis, immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic Query Match 84.3%; Score 738; DB 8; Length 187;  
Best Local Similarity 84.7%; Pred. No. 7e-69;  
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ID AAM95239 standard; protein; 189 AA.  
XX  
AC AAM95239;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE Human reproductive system related antigen SEQ ID NO: 3897.  
KW Human; reproductive system related antigen; reproductive system disorder;  
XX cancer; gene therapy.  
OS Homo sapiens.  
XX  
PN WO200155320-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001339.  
XX  
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Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;	
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ID	AAM43639 standard; protein; 189 AA.
XX	
AC	AAM43639;
XX	
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 317.
XX	
KW	Human; antiarthritic; anti-rheumatic; antiproliferative; vasotropic; cerebrotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human.
XX	
OS	Homo sapiens.
XX	
PN	WO200155308-A2.
XX	
PD	02-AUG-2001.
XX	
PP	17-JAN-2001; 2001WO-US001309.
XX	
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488781/53.
XX N-PSDB; AAI63945.
XX
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating and/or preventing human diseases and disorders.
XX
XX Claim 11; SEQ ID NO 317; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
XX the encoded proteins (AAI634497-AAI63660) useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. The
XX genes were isolated from a range of human tissues disclosed in the
XX specification. The nucleic acids, proteins, antibodies and (ant)agonists
XX are useful in the diagnosis, treatment and prevention of: (a) cancer,
XX e.g. breast and ovarian cancer and other cancers of the adrenal gland,
XX bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
XX urogenital; (b) immune disorders e.g. Addison's disease, allergies,
XX autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
XX wound healing; (e) neurological diseases e.g. cerebral anoxia and
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
XX and parasitic infections. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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XX Sequence 189 AA;
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Best Local Similarity 84.7%; Pred. No. 7.1e-69;
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RESULT 15
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ID AAI63564 standard; protein; 189 AA.
XX
XX AAI63564;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 242.
XX
XX Human; antiarthritic; antirheumatic; antiproliferative; vasotrophic;
XX cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
XX fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
XX neuroprotective; antiallergic; hepatotropic; antidiabetic;
XX antiinflammatory; antitumor; vulnerary; anticonvulsant; antibacterial;
XX antiparasitic; cardiant; gene therapy; cancer; immune disorder;
XX cardiovascular disorder; neurological disease; infection; human.
XX
XX Homo sapiens.
XX
XX WO200155308-A2.
XX
XX 02-AUG-2001.
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XX 17-JAN-2001; 2001WO-US001309.
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XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
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XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-488781/53.  
DR N-PSDB; AAI63870.  
XX  
XX New isolated nucleic acids and polypeptides, useful for diagnosing,  
PT treating and/or preventing human diseases and disorders.  
XX  
XX Claim 11; SEQ ID NO 242; 664pp + Sequence Listing; English.  
XX  
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and  
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating  
CC or ameliorating medical conditions e.g. by protein or gene therapy. The  
CC genes were isolated from a range of human tissues disclosed in the  
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists  
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,  
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,  
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or  
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d)  
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and  
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
CC and parasitic infections. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 189 AA;

Query Match 84.3%; Score 738; DB 4; Length 189;  
Best Local Similarity 84.7%; Pred. No. 7.1e-69;  
Matches 144; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
Qy 1 MGNEASYPLEMCSHFDADKRLQKRRFKKLDLDNSGSLSVVEFMSLPLOQNPVORVID 60  
Db 20 MGNEASYPACMSHFDNDKRLQRRFKKLDLDNSGSLSVVEFMSLPRLRNPVRRVID 79  
Qy 61 IFDTDNGEVDKFEFFIEGVSQFSVKGDKEQKRLRFAFRIDYMDKDGYSNGBLFQVLKQMV 120  
Db 80 VFDTDGDGEVDKFEFFILGTSTQFSVKGDEQKRLRFAFSIYDMDKDGYSNGBLFQVLKQMV 139  
Qy 121 GNNLKDTQLQOIYDKTIINADKDGRIISFEFCVVGGLDIHKQWVDV 170  
Db 140 GNNLTQWLQQLVDKTIILDKDGDGKISFEFSFSAVVRDLRIHKKLVLI 189

Search completed: February 26, 2005, 14:24:52  
Job time : 61.073 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 14:17:13 ; Search time 12.6569 Seconds  
(without alignments)  
1292.323 Million cell updates/sec

Title: US-09-435-257D-35  
Perfect score: 875  
Sequence: 1 MGNEASYPLEMCSHFDADEI.....EEFCVVGGLDIHKRMVVDV 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	875	100.0	170	1	A33391
2	875	100.0	170	1	S34127
3	870	99.4	170	1	JC1220
4	870	99.4	216	1	S42716
5	789	90.2	170	2	JC7242
6	771	88.1	170	2	JC5174
7	767	87.7	170	2	A44307
8	707	80.8	179	2	JC1221
9	704	80.5	176	2	JQ1232
10	704	80.5	369	2	T22708
11	620	70.9	165	2	P80261
12	530.5	60.6	174	2	T47245
13	496	56.7	175	2	JH0462
14	483	55.2	174	2	T41632
15	316.5	36.2	213	2	T31775
16	308.5	35.3	195	2	T28047
17	260	29.7	311	2	T21563
18	233.5	26.7	150	2	T07132
19	233.5	26.7	151	2	A71409
20	230	26.3	591	2	S54788
21	229.5	26.2	149	2	S35187
22	228.5	26.1	149	1	S53006
23	228.5	26.1	149	1	MCP2DC
24	228.5	26.1	149	1	S22503
25	228.5	26.1	149	1	S22971
26	228.5	26.1	149	1	S40301
27	228.5	26.1	149	1	S70768
28	228.5	26.1	149	2	T47417
29	228.5	26.1	149	2	H84667

30	227.5	26.0	149	1	MCBH	calmodulin - barle
31	227.5	26.0	149	1	MCWT	calmodulin - wheat
32	227.5	26.0	149	2	S24952	calmodulin 1 (clon
33	226.5	25.9	149	2	S58311	calmodulin - Biden
34	226.5	25.9	149	2	S80237	calmodulin PCM2/PC
35	225.5	25.8	149	1	MCZQF	calmodulin - malar
36	224.5	25.7	149	1	MCAA	calmodulin - alfal
37	224.5	25.7	149	2	S22860	calmodulin 2 (clon
38	223.5	25.5	149	1	I51202	calmodulin - duck
39	223.5	25.5	149	1	MCCH	calmodulin - chick
40	223.5	25.5	149	1	MCEE	calmodulin - elect
41	223.5	25.5	149	1	MCHU	calmodulin [valida
42	223.5	25.5	149	1	MCRT	calmodulin [valida
43	223.5	25.5	149	2	JC1305	calmodulin - Japan
44	223.5	25.5	149	2	I51402	calmodulin - Afric
45	223.5	25.5	149	2	S37707	calmodulin - mouse

ALIGNMENTS

RESULT 1

A33391

calcineurin regulatory chain - human

N:Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phospho

C:Species: Homo sapiens (man)

C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-Jul-2004

C:Accession: A33391

R:Guerini, D.; Krinke, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.

DNA 8, 675-682, 1989

A:Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-bind

A:Reference number: A33391; MUID:90126237; PMID:2558868

A:Accession: A33391

A:Molecule type: mRNA

A:Residues: 1-170 <GUE>

A:Cross-references: UNIPROT:P06705; GB:M30773; NID:g180704; PID:AAB08721.1; PID:g180705

C:Genetics:

A:Gene: GDB:PPP3R1; CALNB

A:Cross-references: GDB:l36804; OMIM:601302

A:Map position: 2p16-2p15

C:Complex: heterodimer with calcineurin catalytic chain

C:Superfamily: calmodulin; calmodulin repeat homology

C:Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop

F:2-170/Product: calcineurin regulatory chain #status predicted <MAT>

F:18-49/Domain: calmodulin repeat homology <EF1>

F:50-82/Domain: calmodulin repeat homology <EF2>

F:87-119/Domain: calmodulin repeat homology <EF3>

F:128-160/Domain: calmodulin repeat homology <EF4>

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3/Modified site: aspartic acid (Asn) #status predicted

F:31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted

F:63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted

F:100,102,104,106,111/Binding site: calcium (Asp, Asp, Tyr, Arg, Glu) #status predicted

F:141,143,145,147,152/Binding site: calcium (Asp, Asp, Arg, Glu) #status predicted

Query Match 100.0%; Score 875; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 3e-56;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNEASYPLEMCSHFDADEIKRLGKRFKCLDLNLSGSLSVVEEFMSLPQLQNPVQRVID 60

Db 1 MGNEASYPLEMCSHFDADEIKRLGKRFKCLDLNLSGSLSVVEEFMSLPQLQNPVQRVID 60

Qy 61 IFDTGNGEVDKFEFIEGVSVQSVKQKQKLRPAFRFYDMKDGYSNGBELFQVLKQMV 120

Db 61 IFDTGNGEVDKFEFIEGVSVQSVKQKQKLRPAFRFYDMKDGYSNGBELFQVLKQMV 120

Qy 121 GNNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVGGLDIHKRMVVDV 170

Db 121 GNNLKDTQLQOIYDKTIINADKDGGRISFEFCVAVGGLDIHKRMVVDV 170

RESULT 2









```

A;Accession: PS0261
A;Molecule type: mRNA
A;Residues: 1-165 <SUG>
A;Cross-references: GB:S63991; NID:g238643; PIDN:AAB20281.1; PID:g238644
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: blocked amino end; calcium binding; duplication; EF hand
F;7-38/Domain: calmodulin repeat homology <EF1>
F;39-71/Domain: calmodulin repeat homology <EF2>
F;76-108/Domain: calmodulin repeat homology <EF3>
F;117-149/Domain: calmodulin repeat homology <EF4>

Query Match          70.9%; Score 620; DB 2; Length 165;
Best Local Similarity 82.4%; Pred. No. 6.4e-38;
Matches 122; Conservative 12; Mismatches 14; Indels 0; Gaps 0

Qy 23 LGRKFKLLDLNSGSLSEVEFMSLPQLQONPLVQRVIDIFDTDNGGEVDKFKEFIEGVSP 82
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 83 SVKGDKEQKLRFAPRIYDMDKGYISNGELFOVLKQMVGNLKTQLOQIVDKTTINADK 142
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 72 SVRGDEEQKLRFAPRIYDMDNDGFTSNGELFOVLKQMVGNLKDQLQQLVDSILVLDK 131
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 143 DGDGRISFEFECVGGLDIHKKMWVDV 170
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 132 DGDGRISFEFPRDVRVTWEIHKLVVF 159
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
T47245
calcineurin regulatory chain [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47245
R;Dieminger, M.; Tropechug, M.
submitted to the EMBL Data Library, April 1997
A;Reference number: Z24421
A;Accession: T47245
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-174 <DIE>
A;Cross-references: UNIPROT:P87072; EMBL:Y12814; PIDN:CAA73345.1
A;Experimental source: strain 74 A
C;Genetics:
A;Gene: Can B
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand

Query Match          60.6%; Score 530.5; DB 2; Length 174;
Best Local Similarity 63.0%; Pred. No. 1.9e-31;
Matches 105; Conservative 28; Mismatches 36; Indels 3; Gaps 2

Qy 1 MGN-EASVP--LEMCSHFDADIKELGRFKKLKLDNSGSLSEVEFMSLPQLQONPLVQR 57
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 MGNTTSSVPDNIVOGNSFDREVDRLRFRFKLKDQNSGTTIERBEFLSLPQISTNPLATR 60
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 58 VIDIFDTDNGGEVDKFKEFIEGVSPSVKGDKEQKLRFAPRIYDMDKGYISNGELFOVLK 117
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 MIALFDENGGDVDVFQEFVSGLSAFSRKGNKEQKLRFAPKVVYDIDRDGYISNGELFIVLK 120
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 118 MMVGNLKTQLOQIVDKTTINADKDGGRISFEFECVAVGGLDIHKKMWVD 169
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 MMVGNLKDQLOQIVDKTTIMEADLDKGGKISFEFETKQVNTDYSMSMTLD 172
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 13  
JH0462  
phosphoprotein phosphatase regulatory chain - yeast (*Saccharomyces cerevisiae*)  
N:Alternate names: calcineurin chain B homolog; protein phosphatase 2B chain B; protein C; Species: *Saccharomyces cerevisiae*  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: JH0462; A45021; S33962; S38022; S34680; S52282  
R:Kuno, T.; Tanaka, H.; Mukai, H.; Chang, C.D.; Hiraoka, K.; Miyakawa, T.; Tanaka, C.

Biochem. Biophys. Res. Commun. 180, 1159-1163, 1991

A;Title: cDNA cloning of a calcineurin B homolog in Saccharomyces cerevisiae.

A;Reference number: JH0462; MUID:92062059; PMID:1659397

A;Accession: JH0462

A;Molecule type: mRNA

A;Residues: 1-175 <KUN>

A;Cross-references: UNIPROT:P25296; EMBL:D10293; NID:g218409; PIDN:BAA01136.1; PID:g2184

R;Cyert, M.S.; Thorner, J.

Mol. Cell. Biol. 12, 3460-3469, 1992

A;Title: Regulatory subunit (CNB1 gene product) of yeast Ca<sup>2+</sup>/calmodulin-dependent phosph

A;Reference number: A45021; MUID:92334345; PMID:1321337

A;Accession: A45021

A;Molecule type: DNA

A;Residues: 1-175 <CVB>

A;Cross-references: EMBL:M87508; NID:g171250; PIDN:AAA34505.1; PID:g171251

A;Note: sequence extracted from NCBI backbone (NCBIN:108731, NCBIP:108732)

R;Cheret, G.; Mattheakis, L.C.; Sor, F.

Yeast 9, 661-667, 1993

A;Title: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cere

A;Reference number: S33960; MUID:93348778; PMID:8394042

A;Accession: S33962

A;Molecule type: DNA

A;Residues: 1-175 <CHE>

A;Cross-references: GB:X59765; NID:g296985; PIDN:CAA49421.1; PID:g296988

A;Experimental source: strain S288C

R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Senses, C.; Stegemann, J.

submitted to the Protein Sequence Database, March 1994

A;Reference number: S37825

A;Accession: S38022

A;Molecule type: DNA

A;Residues: 1-175 <WIE>

A;Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190W

A;Experimental source: strain S288C

R;Maia e Silva, A.; Bossler, P.; Villela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; R

submitted to the Protein Sequence Database, March 1994

A;Reference number: S38024

A;Accession: S38027

A;Molecule type: DNA

A;Residues: 1-175 <MAI>

A;Cross-references: EMBL:Z28190; NID:g486336; PIDN:CAA82034.1; PID:g486337; MIPS:YKL190W

A;Experimental source: strain S288C

R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grothues

submitted to the EMBL Data Library, July 1993

A;Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome X

A;Reference number: S34679

A;Accession: S34680

A;Molecule type: DNA

A;Residues: 31-175 <W12>

A;Cross-references: EMBL:X74151; NID:g450365; PIDN:CAA52248.1; PID:g395235

A;Experimental source: strain S288C

R;Pardo, J.M.

submitted to the EMBL Data Library, September 1993

A;Description: The protein phosphatase calcineurin is essential for NaCl tolerance in Sa

A;Reference number: S52281

A;Accession: S52282

A;Molecule type: DNA

A;Residues: 1-175 <PAR>

A;Cross-references: EMBL:Z26521; NID:g473144; PIDN:CAA81290.1; PID:g473146

C;Genetics:

A;Gene: SGD:CNB1; YCN2

A;Cross-references: SGD:S0001673; MIPS:YKL190W

A;Map position: 11L

A;Introns: 18/1

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipop

F;2-175/Product: phosphoprotein phosphatase regulatory chain #status predicted <MAT>

F;21-52/Domain: calmodulin repeat homology <EF1>

F;53-85/Domain: calmodulin repeat homology <EF2>

F;90-122/Domain: calmodulin repeat homology <EF3>

F;121-163/Domain: calmodulin repeat homology <EF4>

F;12/Modified site: myristylated amino end (Gly) (in mature form) #status experimental

Query Match 56.7% Score 496; DB 2; Length 175;

### Query Match



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2005, 14:05:22 ; Search time 58.073 Seconds  
(without alignments)  
1499.035 Million cell updates/sec

Title: US-09-435-257D-35  
Perfect score: 875  
Sequence: 1 MGNRASYPLEMCSHPDADEI.....BEFCAVGGGLIHKKQVVVDV 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	875	100.0	170	Q6GH20	Q6gh20 brachydanio
2	875	100.0	170	Q6DJJ3	Q6dj33 xenopus lae
3	875	100.0	170	Q6VN50	Q6vn50 xenopus tro
4	875	100.0	170	Q6VN51	Q6vn51 gallus gall
5	870	99.4	169	1 CALB_BOVIN	P63099 bos taurus
6	870	99.4	169	1 CALB_HUMAN	P63098 homo sapien
7	870	99.4	169	1 CALB_RAT	P63100 rattus norv
8	865	98.9	169	1 CALB_MOUSE	Q63810 mus musculu
9	865	98.9	170	Q7T063	Q7t063 xenopus lae
10	796	91.0	170	Q9NKW7	Q9nk7 patinopecte
11	795	90.9	765	Q86YQ0	Q86yq0 homo sapien
12	771	88.1	170	1 CALC_DROME	Q24214 drosophila
13	769	87.9	169	Q7PQ91	Q7pq91 anopheles g
14	767	87.7	170	1 CALB_DROME	P48451 drosophila
15	767	87.7	170	Q95P81	Q95p81 bombyx mori
16	739.5	84.5	169	Q86H16	Q86h16 schistosoma
17	737.5	84.3	169	Q9NFN1	Q9nfn1 schistosoma
18	733	83.8	169	1 CALC_HUMAN	Q96123 homo sapien
19	709	81.0	171	Q20804	Q20804 caenorhabdi
20	707	80.8	170	Q7YRC9	Q7yrc9 macaca mula
21	702	80.2	178	1 CALC_MOUSE	Q63811 mus musculu
22	699	79.9	175	1 CALC_RAT	P28470 rattus norv
23	580	66.3	115	Q99LQ9	Q99lq9 mus musculu
24	545.5	62.3	174	1 CALB_NEUCR	P87072 neurospora
25	544	62.2	173	1 CALB_YARLI	Q6cge6 yarrowia li
26	528	60.3	175	1 CALB_CRYNE	Q9hdel cryptococu
27	517	59.1	177	1 CALB_NAEGR	P42322 naegleria g
28	501.5	57.3	175	1 CALB_ASHGO	Q757b7 ashbya goss
29	496	56.7	174	1 CALB_YEAST	P25296 saccharomyc
30	483	55.2	174	1 CALB_SCHPO	Q9uu93 schistosacch
31	483	55.2	175	1 CALB_CANGA	Q6flu4 candida gla

32	475	54.3	175	1	CALB_KLULA	Q874t7 kluyveromyc
33	470.5	53.8	174	1	CALB_DEBHA	Q6bwe8 debaryomyc
34	452.5	51.7	177	2	Q8MOT6	Q8mct6 toxoplasma
35	446	51.0	180	2	Q8GP83	Q8gp83 dictyostell
36	445	50.9	169	2	Q867N3	Q867n3 paramecium
37	436.5	49.9	177	2	Q86RA7	Q86ra7 plasmodium
38	436	49.8	179	2	Q8IKV9	Q8ikv9 plasmodium
39	415.5	47.5	166	2	Q7RP38	Q7rp38 plasmodium
40	372	42.5	175	2	Q9UOX7	Q9uox7 leishmania
41	340.5	38.9	194	1	CHP1_MOUSE	P61022 mus musculu
42	340.5	38.9	194	1	CHP1_RAT	P61023 rattus norv
43	338.5	38.7	193	2	Q6DK70	Q6dk70 xenopus tro
44	338.5	38.7	193	2	Q6DKL7	Q6dkl7 xenopus lae
45	337.5	38.6	194	1	CHP1_HUMAN	Q99653 homo sapien

ALIGNMENTS

RESULT 1  
Q6GH20 PRELIMINARY; PRT; 170 AA.  
AC Q6GH20;  
DT 25-OCT-2004 (TRENBLrel. 28, Created)  
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE Zgc:92169.  
GN Name=zgc:92169;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole;  
RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield V.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Maira M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole;  
RA Director MGC Project;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
EMBL; BC081617; AAH81617.1; -  
DR InterPro; IPR001751; CAP\_S100.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF-hand like.  
DR InterPro; IPR008080; Parvalbumin.  
DR InterPro; IPR001125; Recoverin.  
DR Pfam; PF00036; ehand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR ProDom; PD003407; CAP\_S100; 1.  
DR ProDom; PD000012; EF-hand; 2.

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DR SMART: SM00054; EFh: 4.  
DR PROSITE: PS00018; EF HAND: 4.  
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;  
  
Query Match 100.0%; Score 875; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.9e-52;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MGNEASYPLEMCSHFDADKRLGKRFKPKLDLNSGSLSVVEEFMSLPQLQONPLVQRVID 60  
Db 1 MGNEASYPLEMCSHFDADKRLGKRFKPKLDLNSGSLSVVEEFMSLPQLQONPLVQRVID 60  
  
Qy 61 IFPTDGNGEVDKFEFIEGVSVQSVKDGKQKLFKFAFRIVDMDKGYISNGELFQVLKQMV 120  
Db 61 IFPTDGNGEVDKFEFIEGVSVQSVKDGKQKLFKFAFRIVDMDKGYISNGELFQVLKQMV 120  
  
Qy 121 GNNLKDTQLQOIYVDKTIINADKDGGRISFEFCFVAVGGLDIHKKMVVDV 170  
Db 121 GNNLKDTQLQOIYVDKTIINADKDGGRISFEFCFVAVGGLDIHKKMVVDV 170  
  
RESULT 2  
Q6DJJ3 PRELIMINARY; PRT; 170 AA.  
ID Q6DJJ3  
AC Q6DJJ3  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE MGC82148 protein.  
GN Name=MGC82148;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."  
RL Dev. Dyn. 225:384-391(2002).  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Klein S., Gerhard D.S.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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DR PRINTS; PR00450; RECOVERIN.  
DR PrCodm; PD003407; CaBP S100; 1.  
DR PrCodm; PD000012; EF-hand; 2.  
DR SMART; SM00054; EFh; 4.  
DR PRSITE; PS00018; EF HAND; 4.  
KW Calcium; Calcium-binding.  
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 875; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.9e-52;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MGNEASYPLEWCMSHFDADAEIKRLGKRFKKLDLDNGSLSVVEEFMSLPQLQNPVQVRVID 60  
DB 1 MGNEASYPLEWCMSHFDADAEIKRLGKRFKKLDLDNGSLSVVEEFMSLPQLQNPVQVRVID 60  
QY 61 IFTDGNGEVDVDFKEPIEGVSGFSVKGDKEQKLRAFRFYDMDKGYIINGELFQVLKMWV 120  
DB 61 IFTDGNGEVDVDFKEPIEGVSGFSVKGDKEQKLRAFRFYDMDKGYIINGELFQVLKMWV 120  
QY 121 GNNLKDTQLQOIYVDKTIINADKDGGRISPEFCVAVGGDLTHKKMWVDV 170  
DB 121 GNNLKDTQLQOIYVDKTIINADKDGGRISPEFCVAVGGDLTHKKMWVDV 170

RESULT 5

CALB\_BOVIN STANDARD; PRT: 169 AA.

ID P63099; P06705; P15117; Q08044;  
AC 01-JAN-1988 (Rel. 06, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).  
DE 1.  
GN Names=PPP3R1; Synonyms=CNA2, CNB;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
OC NCBI\_TaxId=9913;  
RN [1] TISSUE=Brain;  
RC TISSUE=Brain;  
RX MEDLINE=95102111; PubMed=7803816;  
RA Nargang C.E., Botteroff D.A., Adachi K.;  
RT "Isolation and characterization of a cDNA clone coding for the calcium-binding subunit of calcineurin from bovine brain: an identical amino acid sequence to the human protein.";  
RL DNA Seq. 4:313-318(1994).  
RN [2]  
RP SEQUENCE OF 1-168.  
RP TISSUE=Brain;  
RC MEDLINE=84132092; PubMed=6321184;  
RX Aitken A., Klee C.B., Cohen P.;  
RT "The structure of the B subunit of calcineurin.";  
RL Eur. J. Biochem. 139:663-671(1984).  
RN [3]  
RP CALCIUM-BINDING DATA.  
RP MEDLINE=80101597; PubMed=293720;  
RX Klee C.B., Crouch T.H., Krinks M.H.;  
RA "Calcineurin: a calcium- and calmodulin-binding protein of the nervous system.";  
RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) IN COMPLEX WITH FKBP1A.  
RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;  
RA Griffith J.P., Kim J.L., Kim E.E., Sinterhak M.D., Thomson J.A., Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;  
RT "X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FKBP12-FK506 complex.";  
RL Cell 82:507-522(1995).  
CC -1- FUNCTION: Regulatory subunit of calcineurin. A calcium-dependent.



calmodulin stimulated protein phosphatase. Confers calcium sensitivity.

-1- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory subunit (B).

-1- MISCELLANEOUS: This protein has four functional calcium-binding sites.

-1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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EMBL; X71666; CAA50659.1; -.  
 PDB; 1T00; X-ray; B=1-169.  
 GO; GO:0005955; C:calcineurin complex; NAS.  
 GO; GO:0005509; F:calcium ion binding; NAS.  
 GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.  
 GO; GO:0005517; F:calmodulin inhibitor activity; NAS.  
 InterPro; IPR010983; EF-Hand.  
 InterPro; IPR008080; Parvalbumin.  
 InterPro; IPR001125; Recoverin.  
 Pfam; PF00036; ehand; 4.  
 PRINTS; PR01697; PARVALBUMIN.  
 PRINTS; PR00450; RECOVERIN.  
 PROSITE; PS00018; EF HAND; 4.  
 3D-structure; Calcium-binding; Direct protein sequencing; Lipoprotein; Myristate; Repeat.

INIT MET 0 0  
 LIPID 1 1 N-myristoyl glycine.  
 CA\_BIND 30 41 EF-hand 1.  
 CA\_BIND 62 73 EF-hand 2.  
 CA\_BIND 99 110 EF-hand 3.  
 CA\_BIND 140 151 EF-hand 4.  
 CONFLICT 11 11 C -> M (in Ref. 2).  
 CONFLICT 153 153 C -> S (in Ref. 2).  
 HELIX 16 29  
 TURN 31 32  
 TURN 36 37  
 STRAND 39 42  
 HELIX 43 44  
 TURN 46 49  
 HELIX 50 50  
 TURN 52 53  
 HELIX 54 61  
 TURN 63 64  
 STRAND 69 70  
 TURN 71 78  
 HELIX 79 81  
 TURN 83 84  
 HELIX 87 98  
 TURN 100 101  
 STRAND 105 106  
 TURN 108 119  
 HELIX 120 121  
 TURN 125 139  
 HELIX 141 142  
 TURN 147 148  
 STRAND 149 156  
 HELIX 157 159  
 HELIX 161 164  
 SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;

Query Match 99.4%; Score 870; DB 1; Length 169;  
 Best local similarity 100.0%; Pred. No. 8.5e-52;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 GNEASYPLEMCSHFDADEIKRLGKFKKLDLNSGSLSVSEFMSLPQLQNPLVQVRVIDI 61

Db 1 GNEASYPLEMCSHFDADEIKRLGKFKKLDLNSGSLSVSEFMSLPQLQNPLVQVRVIDI 60  
 Qy 62 FDTGNGEVDFKEFIEGVQSFVKGEQKLFAPRIYMDKDYISNGELFQVLKMMVG 121  
 Db 61 FDTGNGEVDFKEFIEGVQSFVKGEQKLFAPRIYMDKDYISNGELFQVLKMMVG 120  
 Qy 122 NNLDKDTQLQOIIVDKTIINADKDGGRISPEEFCAVVGGLDIHKMVDV 170  
 Db 121 NNLDKDTQLQOIIVDKTIINADKDGGRISPEEFCAVVGGLDIHKMVDV 169

RESULT 6  
 CALB\_HUMAN STANDARD; PRT; 169 AA.  
 AC P63098; P06705; P15117; Q08044;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform 1).  
 GN Name=PPP3R1; Synonyms=CNA2, CNB;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90126237; PubMed=2558868;  
 RA Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;  
 RT "Isolation and sequence of a cDNA clone for human calcineurin B, the Ca2+-binding subunit of the Ca2+/calmodulin-stimulated protein phosphatase.";  
 RL DNA 8:675-682(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
 RT "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201).";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettelman M., Maman A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;  
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A., Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moonaw E.W., Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E., Bacquet R., Villafranca J.E.;  
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-

calcineurin complex.";   
 RL Nature 378:641-644 (1995).   
 [5]   
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) IN COMPLEX WITH PP1A.   
 RX PubMed=12218175; DOI=10.1073/pnas.192206699;   
 RA Huai Q., Kim H.Y., Liu Y., Zhao Y., Mondragon A., Liu J.O., Ke H.;   
 RT "Crystal structure of calcineurin-cyclophilin-cyclosporin shows common   
 but distinct recognition of immunophilin-drug complexes.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12037-12042 (2002).   
 [6]   
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) IN COMPLEX WITH PP1A.   
 RX PubMed=12357034; DOI=10.1073/pnas.212504399;   
 RA Jin L., Harrison S.C.;   
 RT "Crystal structure of human calcineurin complexed with cyclosporin A   
 and human cyclophilin.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13522-13526 (2002).   
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,   
 calmodulin stimulated protein phosphatase. Confers calcium   
 sensitivity.   
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory   
 subunit (B).   
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding   
 sites.   
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.   
 CC   
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 CC -----   
 DR EMBL; M30773; AAB08721.1; -;   
 DR EMBL; BC027913; AAB27913.1; -;   
 DR EMBL; CR456938; CAG33219.1; -;   
 DR PIR; A33391; A33391.   
 DR PDB; 1AUI; X-ray; B=1-169.   
 DR PDB; 1M63; X-ray; B/F=1-169.   
 DR PDB; 1MF8; X-ray; B=1-169.   
 DR OGP; P63098; -   
 DR Genew; HGNC:9317; PPP3R1.   
 DR MIM; 601302; -;   
 DR GO; GO:0005955; C:calcineurin complex; NAS.   
 DR GO; GO:0005909; F:calcium ion binding; NAS.   
 DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.   
 DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.   
 DR InterPro; IPR002048; EF-hand.   
 DR InterPro; IPR010983; EF-hand\_like.   
 DR InterPro; IPR008080; Parvalbumin.   
 DR InterPro; IPR001125; Recoverin.   
 DR Pfam; PF00036; ehand; 4.   
 DR PRINTS; PR01697; PARVALBUMIN.   
 DR PRINTS; PR00450; RECOVERIN.   
 DR PROSITE; PS00018; EF HAND; 4.   
 KW 3D-structure; Calcium-binding; Lipoprotein; Myristate; Repeat.   
 FT INIT MET 0   
 FT LIPID 1   
 FT CA\_BIND 30 41   
 FT CA\_BIND 62 73   
 FT CA\_BIND 99 110   
 FT CA\_BIND 140 151   
 FT HELIX 16 29   
 FT TURN 31 32   
 FT STRAND 36 37   
 FT HELIX 39 42   
 FT TURN 43 44   
 FT HELIX 46 49   
 FT TURN 50 53   
 FT TURN 52 55   
 FT HELIX 54 61   
 FT TURN 63 64   
 FT STRAND 69 70

FT HELIX 71 78   
 FT HELIX 79 81   
 FT TURN 83 84   
 FT HELIX 87 98   
 FT TURN 100 101   
 FT STRAND 105 106   
 FT HELIX 108 119   
 FT TURN 120 121   
 FT HELIX 125 139   
 FT TURN 141 142   
 FT STRAND 147 148   
 FT HELIX 149 156   
 FT HELIX 157 159   
 FT HELIX 161 164   
 SQ SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;   
 Query Match 99.4%; Score 870; DB 1; Length 169;   
 Best Local Similarity 100.0%; Pred. No. 8.5e-52;   
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   
 QY 2 GNEASYPLEMCSHFDADDEIKELGRFKKLDLDSGSLSVSEFMSLPELQQNPLVQRVIDI 61   
 DB 1 GNEASYPLEMCSHFDADDEIKELGRFKKLDLDSGSLSVSEFMSLPELQQNPLVQRVIDI 60   
 QY 62 PDTGNGEVDPKFIEGVSVKDGKEQKLRPAFRIYDMKDGYSINGELFQVLKMWVG 121   
 DB 61 PDTGNGEVDPKFIEGVSVKDGKEQKLRPAFRIYDMKDGYSINGELFQVLKMWVG 120   
 QY 122 NNLKDTOLQIVDKTIINADKDGGRISFEFCFCAVGGGLDTHKMWVDV 170   
 DB 121 NNLKDTOLQIVDKTIINADKDGGRISFEFCFCAVGGGLDTHKMWVDV 169   
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 ID - CALB\_RAT STANDARD; PRT; 169 AA.   
 AC P63100; P06705; P5117; Q08044;   
 DT 01-JAN-1988 (Rel. 06, Created)   
 DT 01-APR-1990 (Rel. 14, Last sequence update)   
 DT 25-OCT-2004 (Rel. 45, Last annotation update)   
 DE Calcineurin B subunit isoform 1 (protein phosphatase 2B regulatory   
 subunit 1) (protein phosphatase 3 regulatory subunit B alpha isoform   
 1).   
 DE Name=Ppp3r1; Synonyms=Cna2, Cnb;   
 OS Rattus norvegicus (Rat).   
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.   
 CX NCBI\_TaxID=10116;   
 RN [1]   
 RP SEQUENCE FROM N.A. (ISOFORM 1).   
 RC STRAIN=Fischer;   
 RA Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;   
 RT "Regulation of calcineurin phosphatase activity by the B subunit and   
 carboxy-terminal inhibitory domains of the A subunit.";   
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.   
 [2]   
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.   
 RC TISSUE=Brain, and Testis;   
 RX MEDLINE=94153993; PubMed=8110831; DOI=10.1016/0167-4781(94)90031-0;   
 RA Chang C.-D., Mukai H., Kuno T., Tanaka C.;   
 RT "cDNA cloning of an alternatively spliced isoform of the regulatory   
 subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin   
 B alpha 2)".   
 RL Biochim. Biophys. Acta 1217:174-180 (1994).   
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,   
 calmodulin stimulated protein phosphatase. Confers calcium   
 sensitivity.   
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory   
 subunit (B).   
 CC -!- ALTERNATIVE PRODUCTS:   
 CC Event=Alternative splicing; Named isoforms=2;   
 CC Name=1;   
 CC IsoId=P63100-1, P06705-1;   
 CC

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CC      Sequence=Displayed;
CC      Name=2;
CC      IsoId=P63100-2, P06705-2;
CC      Sequence=VSP_000729;
CC      -1- TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC      -1- MISCELLANEOUS: This protein has four functional calcium-binding
CC      sites.
CC      -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC      -----
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CC      -----
CC      EMBL; L03554; AAA04854.1; -.
CC      DR      EMBL; D14568; BAA03422.1; -.
CC      DR      EMBL; D14425; BAA03318.1; -.
CC      DR      PIR; S42716; S42716.
CC      DR      RGD; 69230; Ppp3r1.
CC      DR      GO; 0005955; C:calcineurin complex; NAS.
CC      DR      GO; 0005509; F:calcium ion binding; NAS.
CC      DR      GO; 0004723; F:calcium-dependent protein serine/threonine . . .; NAS.
CC      DR      GO; 0005517; F:calmodulin inhibitor activity; NAS.
CC      DR      InterPro; IPR002048; EF-hand.
CC      DR      InterPro; IPR010983; EF-hand like.
CC      DR      InterPro; IPR008080; Parvalbumin.
CC      DR      InterPro; IPR001125; Recoverin.
CC      DR      Pfam; PF00036; ehand; 4.
CC      DR      PRINTS; PR01697; PARVALBUMIN.
CC      DR      PRINTS; PR00450; RECOVERIN.
CC      DR      PROSITE; PS00019; EF_HAND; 4.
CC      DR      PROSITE; PS00018; EF_HAND; 4.
CC      KW      Alternative splicing; Calcium-binding; Lipoprotein; Myristate; Repeat.
CC      FT      INIT MET 0 0 By similarity.
CC      FT      LIPID 1 1 N-myristoyl glycine (By similarity).
CC      FT      CA_BIND 30 41 EF-hand 1.
CC      FT      CA_BIND 62 73 EF-hand 2.
CC      FT      CA_BIND 99 110 EF-hand 3.
CC      FT      CA_BIND 140 151 EF-hand 4.
CC      FT      VARSPLIC 1 1
CC      FT      -----
CC      SQ      SEQUENCE 169 AA; 19169 MW; 749141BD0434C90C CRC64;
CC      -----
CC      Query Match 99.4%; Score 870; DB 1; Length 169;
CC      Best Local Similarity 100.0%; Pred. No. 8.5e-52;
CC      Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC      -----
CC      QY      2 GNEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVLRVIDI 61
CC      DB      1 GNEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVLRVIDI 60
CC      -----
CC      QY      62 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 121
CC      DB      61 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 120
CC      -----
CC      QY      122 NNLKDTQLQOIYVDKTIINADKGDGRISFEFCVAVGGGLDIHKMVDV 170
CC      DB      121 NNLKDTQLQOIYVDKTIINADKGDGRISFEFCVAVGGGLDIHKMVDV 169
CC      -----
CC      RESULT 8
CC      CALB_MOUSE STANDARD; PRT; 169 AA.
CC      AC Q63810;
CC      DT 01-NOV-1997 (Rel. 35, Created)
CC      DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC      DT 25-OCT-2004 (Rel. 45, Last annotation update)
CC      DE Calcineurin B subunit isoform 1 (protein phosphatase 2B regulatory
CC      DE subunit 1) (protein phosphatase 3 regulatory subunit B alpha isoform
CC      DE 1).

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GN      Name=Ppp3r1; Synonyms=Cnb;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=9232379; PubMed=1325794;
RA      Ueki K., Muramatsu T., Kincaid R.L.;
RT      "Structure and expression of two isoforms of the murine calmodulin-
RT      dependent protein phosphatase regulatory subunit (calcineurin B).";
RL      Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC      -1- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
CC      calmodulin stimulated protein phosphatase. Confers calcium
CC      sensitivity.
CC      -1- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
CC      subunit (B).
CC      -1- TISSUE SPECIFICITY: Brain specific.
CC      -1- MISCELLANEOUS: This protein has four functional calcium-binding
CC      sites.
CC      -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; S43864; AAB23171.1; -.
CC      DR      PIR; JC1220; JC1220.
CC      DR      HSP; P06705; IAU1.
CC      DR      MGD; MGI:107172; Ppp3r1.
CC      DR      InterPro; IPR002048; EF-hand.
CC      DR      InterPro; IPR010983; EF-hand like.
CC      DR      InterPro; IPR008080; Parvalbumin.
CC      DR      InterPro; IPR001125; Recoverin.
CC      DR      Pfam; PF00036; ehand; 4.
CC      DR      PRINTS; PR01697; PARVALBUMIN.
CC      DR      PRINTS; PR00450; RECOVERIN.
CC      DR      ProDom; PD003407; CaBP S100; 1.
CC      DR      ProDom; PD000012; EF-hand; 2.
CC      DR      PROSITE; PS00018; EF_HAND; 4.
CC      DR      PROSITE; PS00019; EF_HAND; 4.
CC      KW      Calcium-binding; Lipoprotein; Myristate; Repeat.
CC      FT      INIT MET 0 0 By similarity.
CC      FT      LIPID 1 1 N-myristoyl glycine (By similarity).
CC      FT      CA_BIND 30 41 EF-hand 1.
CC      FT      CA_BIND 62 73 EF-hand 2.
CC      FT      CA_BIND 99 110 EF-hand 3.
CC      FT      CA_BIND 140 151 EF-hand 4.
CC      FT      SEQUENCE 169 AA; 19142 MW; D1490BA5BD2F432F CRC64;
CC      -----
CC      Query Match 98.9%; Score 865; DB 1; Length 169;
CC      Best Local Similarity 99.4%; Pred. No. 1.9e-51;
CC      Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC      -----
CC      QY      2 GNEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVLRVIDI 61
CC      DB      1 GSEASYPLEMCSHFDADEIKRLGKRFKFKLDLDNSGSLSVSEEFMSLPQLQNPVLRVIDI 60
CC      -----
CC      QY      62 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 121
CC      DB      61 FDTDNGEVDFKFEIEGVQSFVKGDKEQKLRFAFRIDYMDKGYISNGELFQVLKQMVG 120
CC      -----
CC      QY      122 NNLKDTQLQOIYVDKTIINADKGDGRISFEFCVAVGGGLDIHKMVDV 170
CC      DB      121 NNLKDTQLQOIYVDKTIINADKGDGRISFEFCVAVGGGLDIHKMVDV 169
CC      -----
CC      RESULT 9
CC      Q7T063

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ID Q7T063 PRELIMINARY; PRT; 170 AA.  
 AC Q7T063;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Protein phosphatase 3 regulatory subunit B alpha isoform type 1  
 DE (Hypothetical protein).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhou G., Li W., Yu L., Zhao S.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 TISSUE=Embryo;  
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 TISSUE=Embryo;  
 RC PubMed=12471932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smalick D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 TISSUE=Embryo;  
 RC Klein S., Gerhard D.S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY336971; AAL6147.1; -;  
 DR EMBL; BC082858; AAG82858.1; -;  
 DR HSSP; P07463; INOY.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR001751; CAP\_S100.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF\_Hand\_like.  
 DR Pfam; PF00036; ehand; 4.  
 DR ProDom; PD003407; CAP\_S100; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR SMART; SM00054; EFh; 4.  
 DR PROSITE; PS00018; EF HAND; 4.  
 DR Calcium; Calcium-binding; Hypothetical protein.  
 KW SEQUENCE 170 AA; 19328 MW; EFDD715DD8A9E956 CRC64;  
 Query Match 98.9%; Score 865; DB 2; Length 170;  
 Best Local Similarity 98.2%; Pred. No. 1.9e-51;  
 Matches 167; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLRVID 60  
 Db |||||  
 QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLRVID 60  
 Db |||||  
 QY 61 IFDTDGNGEVDKFEFIEGVSVKGDKEQKLRFAPRIYDMDKGYISNGELFQVLKQMV 120  
 Db |||||  
 QY 61 IFDTDGNGEVDKFEFIEGVSVKGDKEQKLRFAPRIYDMDKGYISNGELFQVLKQMV 120  
 Db |||||  
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170  
 Db |||||  
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170  
 Db |||||  
 RESULT 10  
 QSNKW7  
 ID Q9NKKW7 PRELIMINARY; PRT; 170 AA.  
 AC Q9NKKW7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Calcineurin B.  
 OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;  
 OC Pectinoidea; Pectinidae; Mizuhopecten.  
 OX NCBI\_TaxID=6573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 TISSUE=Testis;  
 RC Uryu M., Nakatomi A., Watanabe M., Hatause R., Yazawa M.;  
 RT "Molecular Cloning of cDNA Encoding Two Subunits of Calcineurin from  
 RT Scallops: Demonstration of Stage-Specific Expression during  
 RT Maturation of the Testis.";  
 RL J. Biochem. 0:0-0 (2000).  
 DR EMBL; AB041524; BAA94543.1; -;  
 DR PIR; JC7242; JC7242.  
 DR HSSP; P41208; IM39.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF Hand Like.  
 DR InterPro; IPR008080; Parvalbumin.  
 DR InterPro; IPR001125; Recoverin.  
 DR Pfam; PF00036; ehand; 4.  
 DR PRINTS; PR01697; PARVALBUMIN.  
 DR PRINTS; PR00450; RECOVERIN.  
 DR SMART; SM00054; EFh; 4.  
 DR PROSITE; PS00018; EF HAND; 4.  
 DR Calcium; Calcium-binding.  
 KW SEQUENCE 170 AA; 19238 MW; 9450322698470F44 CRC64;  
 Query Match 91.0%; Score 796; DB 2; Length 170;  
 Best Local Similarity 89.4%; Pred. No. 9.2e-47;  
 Matches 152; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLRVID 60  
 Db |||||  
 QY 1 MGNEASYPLEMCSHFDADEIKRLGKRFKGLDLDNSGSLSVVEFMSPLELQNPVLRVID 60  
 Db |||||  
 QY 61 IFDTDGNGEVDKFEFIEGVSVKGDKEQKLRFAPRIYDMDKGYISNGELFQVLKQMV 120  
 Db |||||  
 QY 61 IFDTDGNGEVDKFEFIEGVSVKGDKEQKLRFAPRIYDMDKGYISNGELFQVLKQMV 120  
 Db |||||  
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170  
 Db |||||  
 QY 121 GNNLKDTQLQOI VDKTIINADKDGRI SPFEFCVAVGGLDIHKQMVVDV 170  
 Db |||||  
 RESULT 11  
 Q86YQ0  
 ID Q86YQ0 PRELIMINARY; PRT; 765 AA.  
 AC Q86YQ0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)



RA Celniker S.E.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Calcineurin is a calcium binding and calmodulin binding  
 CC protein found in all cells from yeast to mammals, it is a calcium  
 CC dependent, calmodulin stimulated protein phosphatase (By  
 CC similarity).  
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory  
 CC subunit (B) (By similarity).  
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding  
 CC sites.  
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U56245; AAC47350.1; -;  
 DR EMBL; AE003840; AAF59195.2; -;  
 DR EMBL; AY070642; AAL48113.1; -;  
 DR EMBL; AY089602; AAL90340.1; -;  
 DR EMBL; BT003768; AAO41447.1; -;  
 DR PIR; JC5174; JC5174.  
 DR HSSP; P06705; 1M63.  
 DR FLYBase; FBGN0015614; CanB2.  
 DR GO; GO:0008021; C:synaptic vesicle; NAS.  
 DR GO; GO:0007269; P:neurotransmitter secretion; NAS.  
 DR GO; GO:0016083; P:synaptic vesicle fusion; NAS.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF Hand like.  
 DR InterPro; IPR008080; Parvalbumin.  
 DR InterPro; IPR001125; Recoverin.  
 DR Pfam; PF00036; ehand; 4.  
 DR PRINTS; PR01697; PARVALBUMIN.  
 DR PRODOM; PD000450; RECOVERIN.  
 DR SMART; SM00054; EFh; 4.  
 DR PROSITE; PS00018; EF-hand; 4.  
 DR Calcium-binding; Repeat.  
 DR CA\_BIND 31 42 EF-hand 1 (Potential).  
 FT CA\_BIND 63 74 EF-hand 2 (Potential).  
 FT CA\_BIND 100 111 EF-hand 3 (Potential).  
 FT CA\_BIND 141 152 EF-hand 4 (Potential).  
 FT CONFLICT 10 10 E -> D (in Ref. 4; AAL48113).  
 FT CONFLICT 40 40 V -> I (in Ref. 4; AAL48113).  
 FT CONFLICT 85 85 K -> R (in Ref. 4; AAL48113).  
 FT CONFLICT 138 138 G -> C (in Ref. 4; AAL48113).  
 SQ SEQUENCE 170 AA; 19267 MW; FDB1BD9DB5A4BDEC CRC64;  
 Query Match 88.1%; Score 771; DB 1; Length 170;  
 Best Local Similarity 87.6%; Pred. No. 4.6e-45;  
 Matches 149; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
 Qy 1 MGNESYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQNPVQVRVID 60  
 Db 1 MGNETSLPMELCSNFDADRIIRLGRFKKLDLNSGSLSVVEEFMSLPQLQNPVQVRVID 60  
 Qy 61 IFDTGNGEVDFKFEIEGVSQFSVKGDKEQKLRFAFRFYDMDKGYISNGELFQVLKQMV 120  
 Db 61 IFDADGNGEVDFKFEIEGVSQFSVKGDKSLKLRFAFRFYDMDNDGYISNGELFQVLKQMV 120  
 Qy 121 GNNLKDTQLQIQIVDKTIINADKDGGRISFEEFCVAVVGGLDIHKQWVDV 170  
 Db 121 GNNLKDTQLQIQIVDKTIINADKDEGDKISFDEFCVAVVGNTDIHKQWVDV 170  
 Query Match 87.9%; Score 769; DB 2; Length 169;  
 Best Local Similarity 86.4%; Pred. No. 6.2e-45;  
 Matches 146; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
 Qy 2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQNPVQVRVID 61  
 Db 1 GNETSLPMELCSNFDADRIIRLGRFKKLDLNSGSLSVVEEFMSLPQLQNPVQVRVID 60  
 Qy 62 FDTGNGEVDFKFEIEGVSQFSVKGDKEQKLRFAFRFYDMDKGYISNGELFQVLKQMV 121  
 Db 61 FDADGNGEVDFKFEIEGVSQFSVKGDKSLKLRFAFRFYDMDNDGYISNGELFQVLKQMV 120  
 Qy 122 NNLKDTQLQIQIVDKTIINADKDGGRISFEEFCVAVVGGLDIHKQWVDV 170  
 Db 121 NNLKDTQLQIQIVDKTIIVFADKDEGDKISFDEFCVAVVGNTDIHKQWVDV 169  
 RESULT 14  
 CALB DROME STANDARD; PRT; 170 AA.  
 AC P48451; Q9W4D0;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).  
 GN Name=canb; Synonyms=CANB1, CNB, CNB1; ORFNames=CG4209;  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93054551; PubMed=1331060;  
 RA Guerini D., Montell C., Klee C.B.;  
 RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin."  
 RL J. Biol. Chem. 267:22542-22549 (1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.

DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE ENSANGP0000013463 (ENSANGP00000024230) (Fragment).  
 GN Name=ENSANGG0000010974; PEST.  
 OS Anopheles gambiae str. PEST.  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 CC NCB1\_TaxID=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAB0100898; EAA09157.2; -;  
 DR HSSP; P09860; 1DTL.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR02048; EF-hand.  
 DR InterPro; IPR010983; EF\_Hand\_like.  
 DR InterPro; IPR008080; Parvalbumin.  
 DR InterPro; IPR001125; Recoverin.  
 DR Pfam; PF00036; ehand; 4.  
 DR PRINTS; PR01697; PARVALBUMIN.  
 DR PRODOM; PD000450; RECOVERIN.  
 DR PROSITE; PS00018; EF-hand; 2.  
 DR PROSITE; PS00018; EF\_HAND; UNKNOWN\_4.  
 FT NON TER 1  
 SQ SEQUENCE 169 AA; 19118 MW; D5D18F14C191601B CRC64;  
 Query Match 87.9%; Score 769; DB 2; Length 169;  
 Best Local Similarity 86.4%; Pred. No. 6.2e-45;  
 Matches 146; Conservative 13; Mismatches 10; Indels 0; Gaps 0;  
 Qy 2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQNPVQVRVID 61  
 Db 1 GNETSLPMELCSNFDADRIIRLGRFKKLDLNSGSLSVVEEFMSLPQLQNPVQVRVID 60  
 Qy 62 FDTGNGEVDFKFEIEGVSQFSVKGDKEQKLRFAFRFYDMDKGYISNGELFQVLKQMV 121  
 Db 61 FDADGNGEVDFKFEIEGVSQFSVKGDKSLKLRFAFRFYDMDNDGYISNGELFQVLKQMV 120  
 Qy 122 NNLKDTQLQIQIVDKTIINADKDGGRISFEEFCVAVVGGLDIHKQWVDV 170  
 Db 121 NNLKDTQLQIQIVDKTIIVFADKDEGDKISFDEFCVAVVGNTDIHKQWVDV 169  
 RESULT 14  
 CALB DROME STANDARD; PRT; 170 AA.  
 AC P48451; Q9W4D0;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Calcineurin B subunit, isoform 1 (Protein phosphatase 2B regulatory subunit).  
 GN Name=canb; Synonyms=CANB1, CNB, CNB1; ORFNames=CG4209;  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93054551; PubMed=1331060;  
 RA Guerini D., Montell C., Klee C.B.;  
 RT "Molecular cloning and characterization of the genes encoding the two subunits of Drosophila melanogaster calcineurin."  
 RL J. Biol. Chem. 267:22542-22549 (1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
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RP GENOME REANNOTATION.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
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CC -1- FUNCTION: Calcineurin is a calcium binding and calmodulin binding  
CC protein found in all cells from yeast to mammals, it is a calcium  
CC dependent, calmodulin stimulated protein phosphatase (By  
CC similarity).  
CC  
CC -1- SUBUNIT: Composed of two components (A and B), the A component is  
CC the catalytic subunit and the B component confers calcium  
CC sensitivity (By similarity).  
CC  
CC -1- MISCELLANEOUS: This protein has four functional calcium-binding  
CC sites.  
CC  
CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
CC  
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CC  
CC EMBL; M97215; AAA28411.1; -.  
  
DR EMBL; AE003434; AAP46026.1; -.  
DR F1R; A44307; A44307.  
DR HSP; P06705; IM63.  
DR IntAct; P48451; -.  
DR FlyBase; FBgn0010014; CanB.  
DR GO; GO:0008021; C:synaptic vesicle; NAS.  
DR GO; GO:0007269; P:neurotransmitter secretion; NAS.  
DR GO; GO:0016083; P:synaptic vesicle fusion; NAS.  
DR InterPro; IPRO02048; EF-hand.  
DR InterPro; IPRO10983; EF-hand like.  
DR InterPro; IPRO08080; Parvalbumin.  
DR InterPro; IPRO01125; Recoverin.  
DR Pfam; PF00036; ehand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR ProDom; PD000012; EF-hand; 2.  
DR SMART; SM00054; EFH; 4.  
DR PROSITE; PS00018; EF-HAND; 4.  
KW Calcium-binding; Repeat.  
FT CA\_BIND 31 42 EF-hand 1 (Potential).  
FT CA\_BIND 63 74 EF-hand 2 (Potential).  
FT CA\_BIND 100 111 EF-hand 3 (Potential).  
FT CA\_BIND 141 152 EF-hand 4 (Potential).  
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Best Local Similarity 85.9%; Pctid.No. 8.6e-45;  
Matches 146; Conservative 13; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 MGNEASYPLMCSHFDADEIKRLGKFKKLDLNSGSLSVVEFMSLPELQONPLVQRVID 60  
DB 1 MGNETSLPMDMCSNFDADEIRLKGKFKKLDLNSGSLSVVEFMSLPELQONPLVQRVID 60  
QY 61 IFDTDNGEVDKFEFTGVSQSVKGDKEQKLFAPRIYDMDKDGYISNSELFOVLKQMV 120  
DB 61 IFDADNGEVDKFEFTGVSQSVKGDKEQKLFAPRIYDMDKDGYISNSELFOVLKQMV 120  
QY 121 GNNLKDTQLQOIIVDKTIINADKDGGRISFEERCAVVGGLDIHKMVDV 170  
DB 121 GNNLKDTQLQOIIVDKTIINADKDGGRISFEERCAVVGGLDIHKMVDV 170  
  
RESULT 15  
Q95P81 PRELIMINARY; PRT; 170 AA.  
AC Q95P81;  
DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Calcineurin B.  
GN Namescnb;  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
OC Bombycidae; Bombyx.  
OX NCBI\_TaxID=7091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Shuko x Ryuhaku; TISSUE=Pheromone gland;  
RX MEDLINE=21883861; PubMed=11886782; DOI=10.1016/S0965-1748(01)00125-4;  
RA Yoshiga T., Yokoyama N., Imai N., Ohnishi A., Moto K., Matsumoto S.;  
RT "cDNA cloning of calcineurin heterosubunits from the pheromone gland  
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RL Insect Biochem. Mol. Biol. 32:477-486(2002).  
DR EMBL; AF287251; AAK83039.1; -.  
DR HSP; P41208; IM39.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPRO02048; EF-hand.  
DR InterPro; IPRO10983; EF-hand like.  
DR InterPro; IPRO08080; Parvalbumin.  
DR InterPro; IPRO01125; Recoverin.  
DR Pfam; PF00036; ehand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.

DR PRINTS; PRO0450; RECOVERIN.  
DR SMART; SMO0054; EFH; 4.  
DR PROSITE; PS00018; EF HAND; UNKNOWN 4.  
SQ SEQUENCE 170 AA; 19357 MW; 5EC15B820097130 CRC64;  
Query Match 87.7%; Score 767; DB 2; Length 170;  
Best Local Similarity 86.5%; Pred. No. 8.6e-45;  
Matches 147; Conservative 12; Mismatches 11; Indels 0; Gaps 0;  
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Db 1 MGNESVPLEMCSHFDADEIRLGRPKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVID 60  
Qy 61 IFDTDGNGEVDFKEFIEGVQSVKGDKEQKLRFAFRIYDMDKGYISNGELFQVLKMMV 120  
Db 61 IFDADGNGEVDFKEFIEGVQSVKGDKLSKLRFAFRIYDMNDGFIENGELFQVLKMMV 120  
Qy 121 GNNLKDQLOQIVDKTIINADKDGGRISFEFCVVGGLDIHKMMVVDV 170  
Db 121 GNNLKDQLOQIVDKTILFADKDEGKISFEFCVVGNTDIHKMMVVDV 170

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